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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 08:17:54 ; Search time 23433 Seconds
(without alignments)
17657.111 Million cell updates/sec

Title: US-09-275-883-1_COPY_1_8539
Perfect score: 8539
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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4: gb_om:*
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6: gb_pat:*
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8: gb_pl:*
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10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8539	100.0	11282	6	BD203630	BD203630 Inducible
2	8539	100.0	11282	6	CQ790428	CQ790428 Sequence
3	8539	100.0	11282	6	AR342585	AR342585 Sequence
4	8539	100.0	11282	6	AX128601	AX128601 Sequence
5	8539	100.0	11282	6	AX174827	AX174827 Sequence
6	7657.2	89.7	13068	6	CQ790429	CQ790429 Sequence
7	7657.2	89.7	15081	6	CQ790448	CQ790448 Sequence
8	7657.2	89.7	17753	6	CQ790449	CQ790449 Sequence
9	7637.4	89.4	9951	6	AR282858	AR282858 Sequence
10	7637.4	89.4	9951	6	AX128602	AX128602 Sequence
11	7637.4	89.4	10524	6	AR282859	AR282859 Sequence
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13	7637.4	89.4	13905	6	AR137241	AR137241 Sequence
14	7637.4	89.4	13905	6	AR282856	AR282856 Sequence
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19	7634.8	89.4	8000	6	AR353270	AR353270 Sequence
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21	7634.8	89.4	8000	6	BD085671	BD085671 Recombina
22	7634.8	89.4	11703	14	SINCG	J02363 Sindbis vir
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24	7634.8	89.4	11740	6	AR230677	AR230677 Sequence
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31	7620.4	89.2	11703	6	BD269911	BD269911 Compositi
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38	7617.2	89.2	8000	6	AR234149	AR234149 Sequence
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45	7612.4	89.1	16656	6	AR062299	AR062299 Sequence

ALIGNMENTS

RESULT 1
BD203630
LOCUS BD203630 11282 bp DNA linear PAT 17-JUL-2003
DEFINITION Inducible alpha virus gene expression system.
ACCESSION BD203630
VERSION BD203630.1 GI:33013400
KEYWORDS JP 2002509729-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 11282)
AUTHORS Renner,W.A., Nieba,L. and Boorsma,M.
TITLE Inducible alpha virus gene expression system
JOURNAL Patent: JP 2002509729-A 1 02-APR-2002;
CYTOS BIOTECHNOLOGY AG
COMMENT OS Artificial Sequence
PN JP 2002509729-A/1
PD 02-APR-2002
PF 25-MAR-1999 JP 2000541320
PR 27-MAR-1998 US 60/079562
PI WOLFGANG A RENNER,LARS NIEBA,MARCO BOORSMA
PC C12N15/09,A01K67/027,A61K48/00,C07K14/18,C12N1/15,C12N1/19, PC C12N1/21,
PC C12N5/10,C12N7/04,C12N9/12,C12N15/00,C12N5/00 CC Description of Artificial Sequence:cDNA
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FT source 1. .11282
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .11282
/organism="synthetic construct"
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ORIGIN

Query Match 100.0%; Score 8539; DB 6; Length 11282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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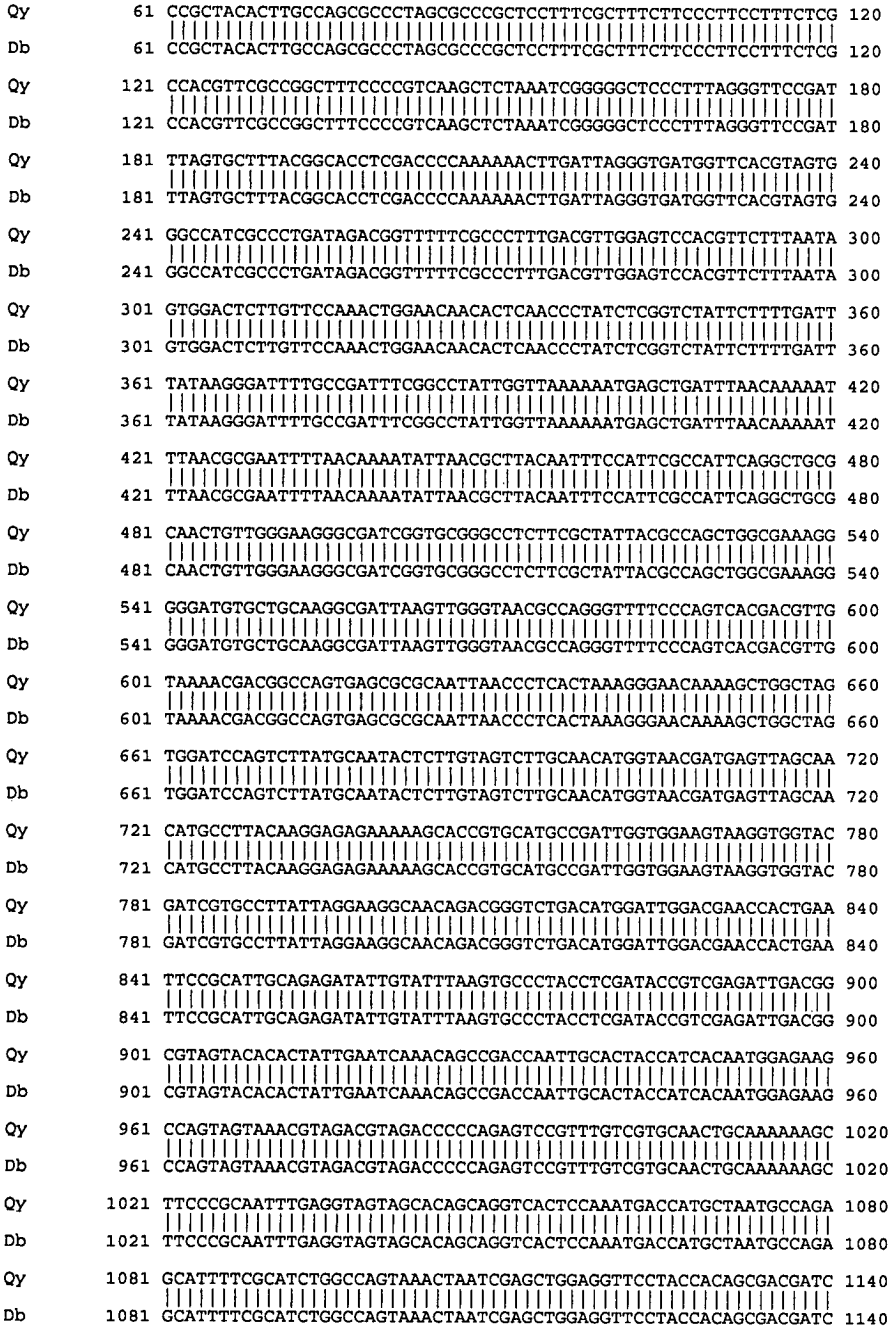
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Qy       4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680
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Qy       6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300
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RESULT 2
CQ790428
LOCUS       CQ790428               11282 bp    DNA     linear   PAT 29-MAR-2004
DEFINITION  Sequence 1 from Patent WO2004018506.
ACCESSION   CQ790428
VERSION     CQ790428.1  GI:45823470
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ivanova,L., Renner,W.A. and Saudan,P.
  TITLE     Inducible alphaviral/orip based gene expression system
  JOURNAL   Patent: WO 2004018506-A 1 04-MAR-2004;
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Cytos Biotechnology AG (CH)
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/note="cDNA"
ORIGIN

Query Match 100.0%; Score 8539; DB 6; Length 11282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
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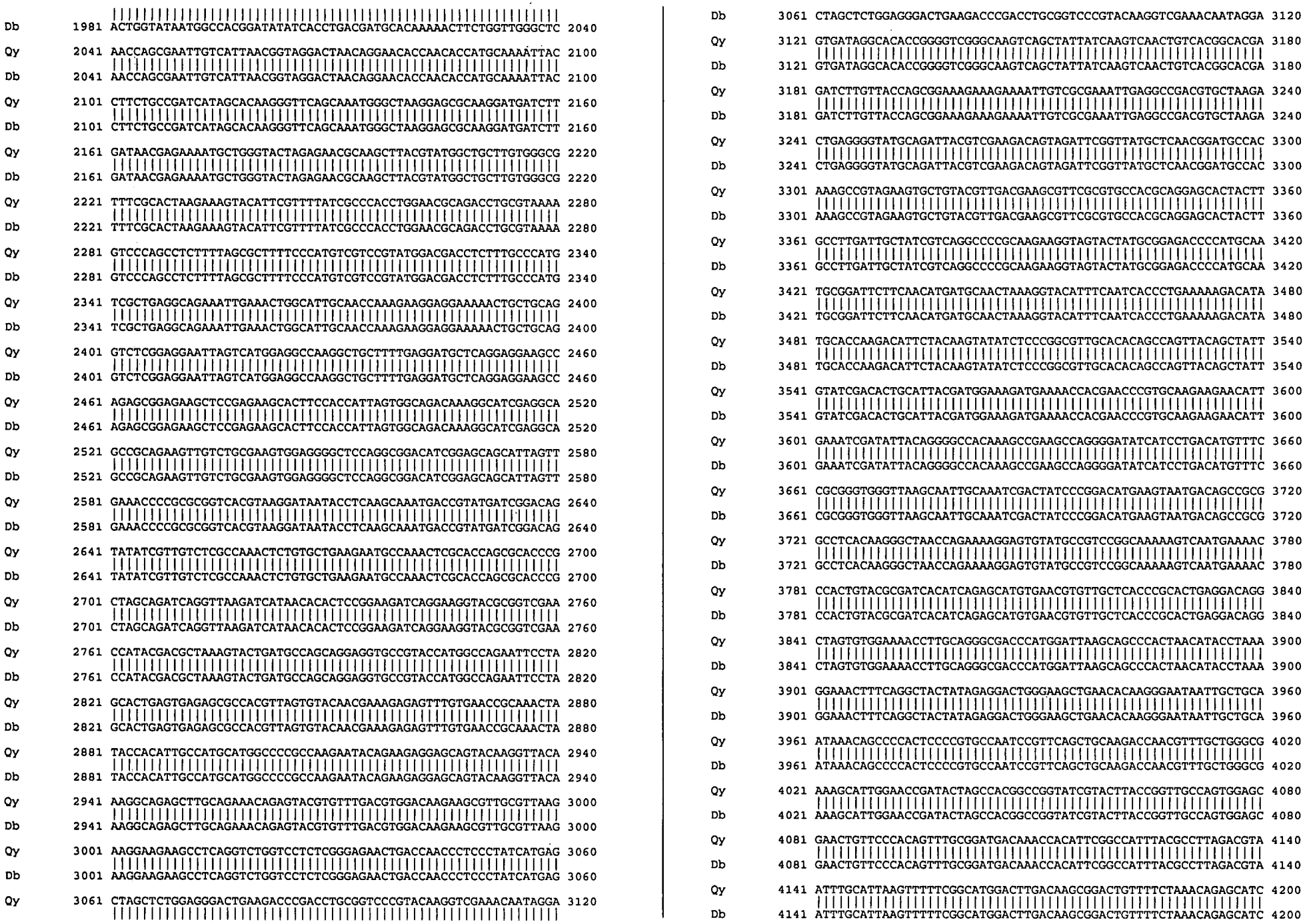
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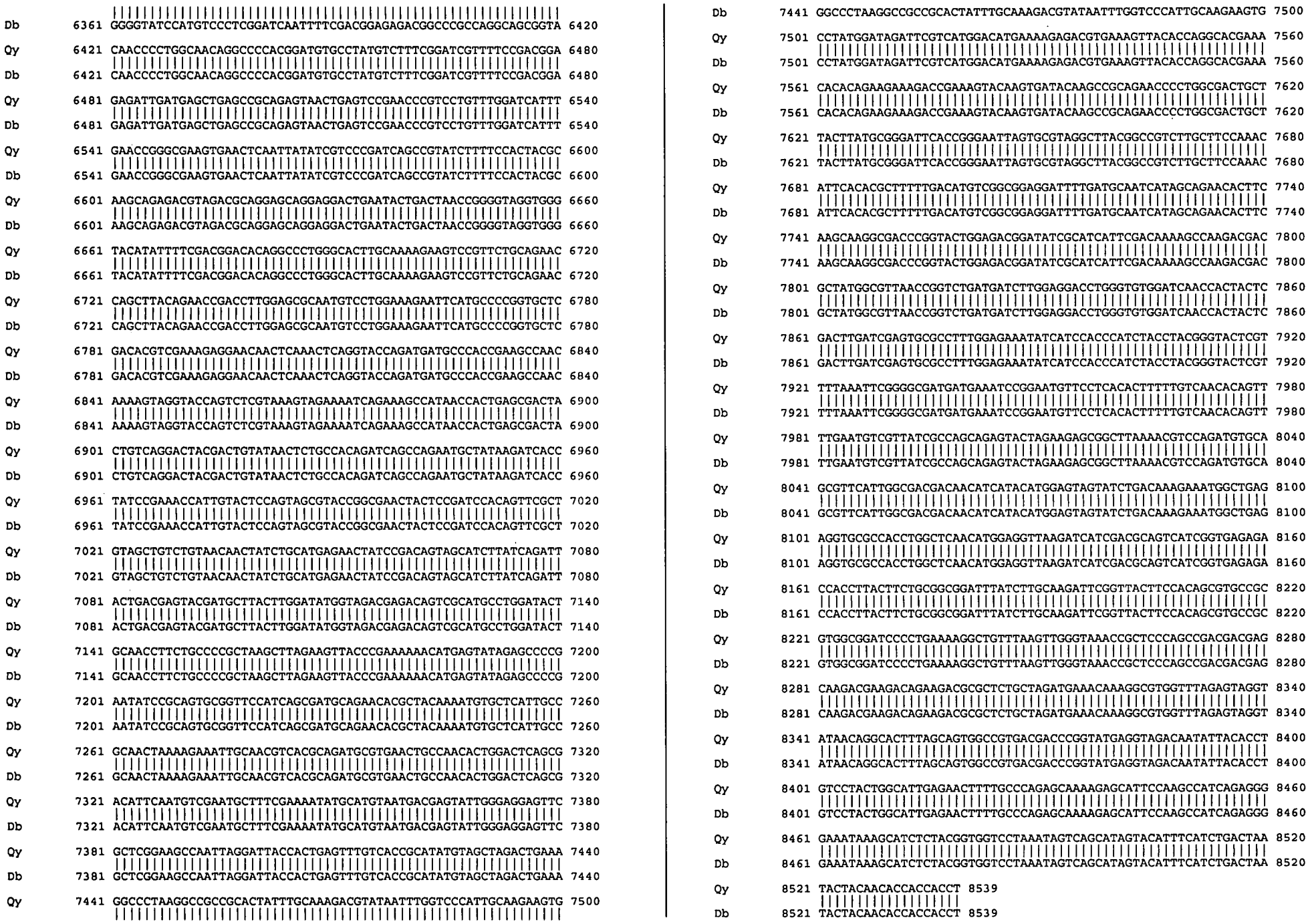
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Db 8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460
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Qy 8521 TACTACAACACCACCACCT 8539
Db 8521 TACTACAACACCACCACCT 8539

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RESULT 3
AR342585
LOCUS       AR342585               11282 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1 from patent US 6576443.
ACCESSION   AR342585
VERSION     AR342585.1  GI:33737767
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11282)
  AUTHORS   Hennecke,F. and Renner,W.A.
  TITLE     Replicon based activation of endogenous genes
  JOURNAL   Patent: US 6576443-A 1 10-JUN-2003;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 8539;  DB 6;  Length 11282;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 8539;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
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Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
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Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
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Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
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Db        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
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Db        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCG 480
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Qy        541 GGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTG 600
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Qy        601 TAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAACAAAAGCTGGCTAG 660
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Qy        661 TGGATCCAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAA 720
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Db        661 TGGATCCAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAA 720

Qy        721 CATGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTAC 780
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Qy        781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAA 840
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Qy        841 TTCCGCATTGCAGAGATATTGTATTTAAGTGCCCTACCTCGATACCGTCGAGATTGACGG 900
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Db        901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960

Qy        961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020
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Qy       1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080
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Qy       1141 TTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATTGTGTC 1200
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Qy       1381 AACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCGGAACTATC 1440
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Qy       1801 GAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAACCGTGGGA 1860
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Qy       1921 GGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCGATCAGATG 1980
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Qy       2041 AACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGCAAAATTAC 2100
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Qy       2701 CTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACGCGGTCGAA 2760
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Qy       2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940
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Db       2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940

Qy       2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000
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Db       2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000

Qy       3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060
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Qy       3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
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Db       3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240

Qy       3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300
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Db       3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360

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Qy       3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660

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Db       3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780

Qy       3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840
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Db       3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840

Qy       3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900

Qy       3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960

Qy       3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
Qy      4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
Qy      4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140
Qy      4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200
Qy      4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260
Qy      4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320
Qy      4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380
Qy      4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440
Qy      4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500
Qy      4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560
Qy      4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620
Qy      4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680
Qy      4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740
Qy      4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800
Qy      4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860
Qy      4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920
Qy      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980
Qy      4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040
Qy      5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100

Qy      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160
Qy      5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220
Qy      5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280
Qy      5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340
Qy      5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400
Qy      5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460
Qy      5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520
Qy      5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580
Qy      5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640
Qy      5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700
Qy      5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760
Qy      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820
Qy      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880
Qy      5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940
Qy      5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000
Qy      6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060
Qy      6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120
Qy      6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180
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Qy       6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240

Qy       6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300

Qy       6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360

Qy       6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420

Qy       6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480

Qy       6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540

Qy       6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600

Qy       6601 AAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGGTAGGTGGG 6660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6601 AAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGGTAGGTGGG 6660

Qy       6661 TACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTCTGCAGAAC 6720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6661 TACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTCTGCAGAAC 6720

Qy       6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCCCGGTGCTC 6780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCCCGGTGCTC 6780

Qy       6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840

Qy       6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900

Qy       6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960

Qy       6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020

Qy       7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080

Qy       7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140

Qy       7141 GCAACCTTCTGCCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200

Qy       7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260

Qy       7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320

Qy       7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380

Qy       7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440
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Db       7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440

Qy       7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500

Qy       7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560

Qy       7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620

Qy       7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680

Qy       7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740

Qy       7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800

Qy       7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
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Db       7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860

Qy       7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920

Qy       7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980

Qy       7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040

Qy       8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100

Qy       8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160

Qy       8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220

Qy       8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280

Qy       8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340

Qy       8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400
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Db       8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400

Qy       8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460
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RESULT 4
AX128601
LOCUS       AX128601               11282 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 1 from Patent WO0130989.
ACCESSION   AX128601
VERSION     AX128601.1  GI:14135063
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Renner,W.A. and Nieba,L.
  TITLE     Method for creating divergent populations of nucleic acid molecules
            and proteins
  JOURNAL   Patent: WO 0130989-A 1 03-MAY-2001;
            Cytos Biotechnology AG (CH) ; Renner, Wolfgand Andreas (CH) ;
            Nieba, Lars (CH)
FEATURES             Location/Qualifiers
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                     /note="vector"
ORIGIN

  Query Match             100.0%;  Score 8539;  DB 6;  Length 11282;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 8539;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
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Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
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Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
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Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCG 480
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Qy      3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
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Db      3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
Qy      3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
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Qy      4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920
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Db      4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920

Qy      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980
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Db      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980

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Qy      5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100
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Qy      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160
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Qy      5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220
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Qy      5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280
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Qy      5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340
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Qy      5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400
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Qy      5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460
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Db      5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460

Qy      5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520
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Db      5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520

Qy      5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580
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Qy      5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640
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Qy      5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700
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Qy      5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760
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Qy      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820
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Db      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820

Qy      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880
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Db      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880

Qy      5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940
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Db       5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940

Qy       5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000
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Qy       6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060
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Qy       6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180
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Qy       6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300
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Qy       6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360
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Qy       6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480
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Db       6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480

Qy       6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540
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Db       6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540

Qy       6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600
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Qy       6601 AAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGGTAGGTGGG 6660
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Qy       6661 TACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTCTGCAGAAC 6720
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Qy       6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCCCGGTGCTC 6780
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Qy       6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840
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Db       6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840

Qy       6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900
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Db       6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900

Qy       6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960
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Qy       7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
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Qy       7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200
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Db       7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200

Qy       7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260
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Qy       7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
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Qy       7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
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Qy       8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160
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Qy       8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220
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Qy       8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460
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RESULT 5
AX174827
LOCUS       AX174827               11282 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 1 from Patent WO0142442.
ACCESSION   AX174827
VERSION     AX174827.1  GI:14598323
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Hennecke,F. and Renner,W.A.
  TITLE     Activation of endogenous genes by genomic introduction of a
            replicon
  JOURNAL   Patent: WO 0142442-A 1 14-JUN-2001;
            Cytos Biotechnology AG (CH)
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ORIGIN
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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 8539;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
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Db         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
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Db        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
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Qy         181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
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Db         181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240

Qy         241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
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Qy         361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
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Qy         661 TGGATCCAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAA 720
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Qy         721 CATGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTAC 780
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Qy         781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAA 840
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Db         781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAA 840

Qy         841 TTCCGCATTGCAGAGATATTGTATTTAAGTGCCCTACCTCGATACCGTCGAGATTGACGG 900
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Qy         901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960
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Qy         961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080

Qy        1081 GCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGACGATC 1140
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Db        1081 GCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGACGATC 1140

Qy        1141 TTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATTGTGTC 1200
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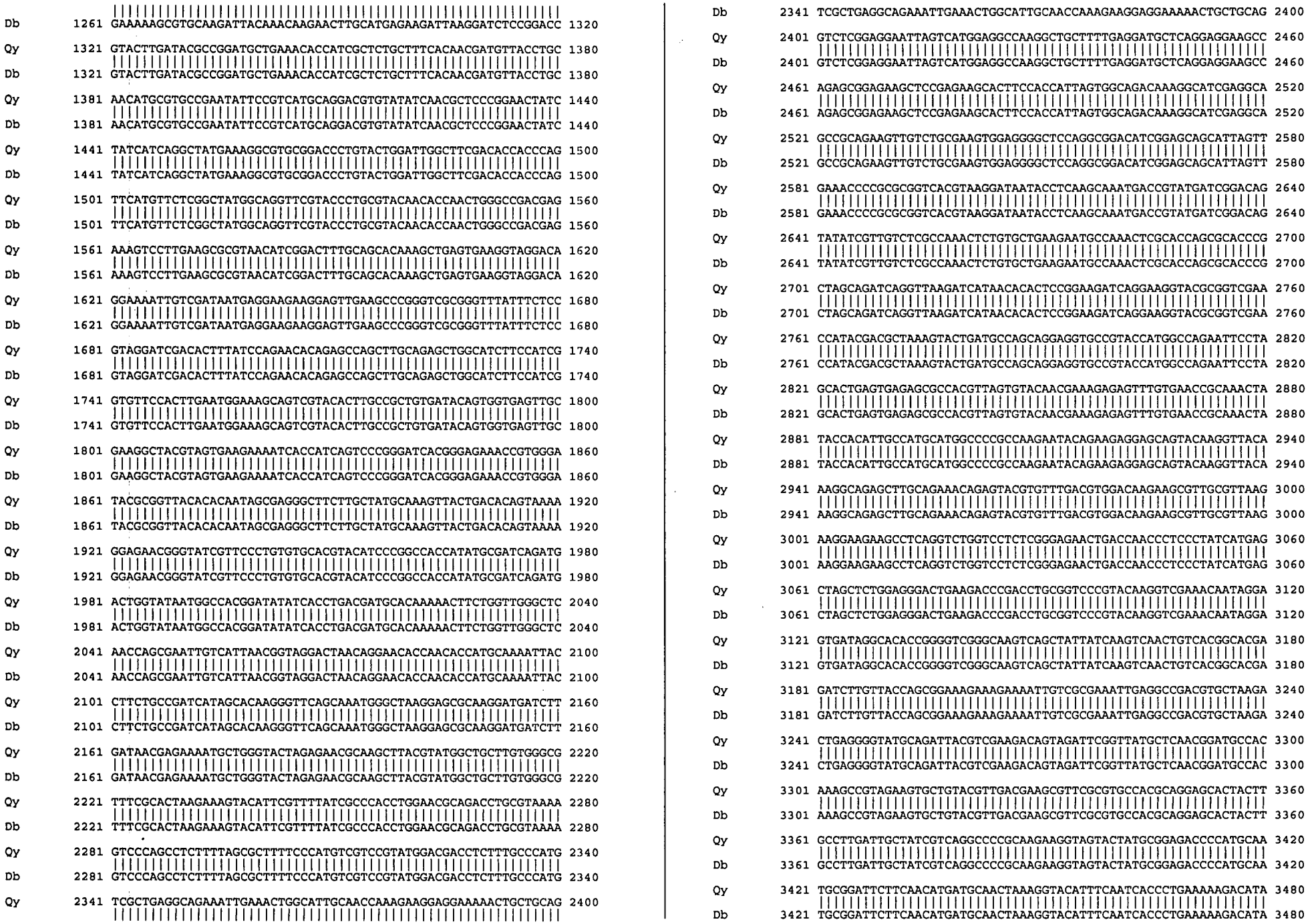

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Qy      3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
Db      3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600

Qy      3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660
Db      3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660

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Qy      4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440
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Qy      4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500
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Qy      4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560
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Qy      4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620
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Qy      4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740
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Qy      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980
Db      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980

Qy      4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040
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Qy      5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100
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Qy      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160
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Qy      5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220
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Qy      5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280
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Qy      5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340
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Qy      5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400
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Qy      5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460
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Qy      5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520
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Qy      5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580
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Qy       6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360
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RESULT 6
CQ790429
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KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ivanova,L., Renner,W.A. and Saudan,P.
  TITLE     Inducible alphaviral/orip based gene expression system
  JOURNAL   Patent: WO 2004018506-A 2 04-MAR-2004;
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ORIGIN
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Query Match           89.7%;  Score 7657.2;  DB 6;  Length 13068;
Best Local Similarity  99.9%;  Pred. No. 0;
Matches 7642;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

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Db        869 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 928

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
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Db        989 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1048

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Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
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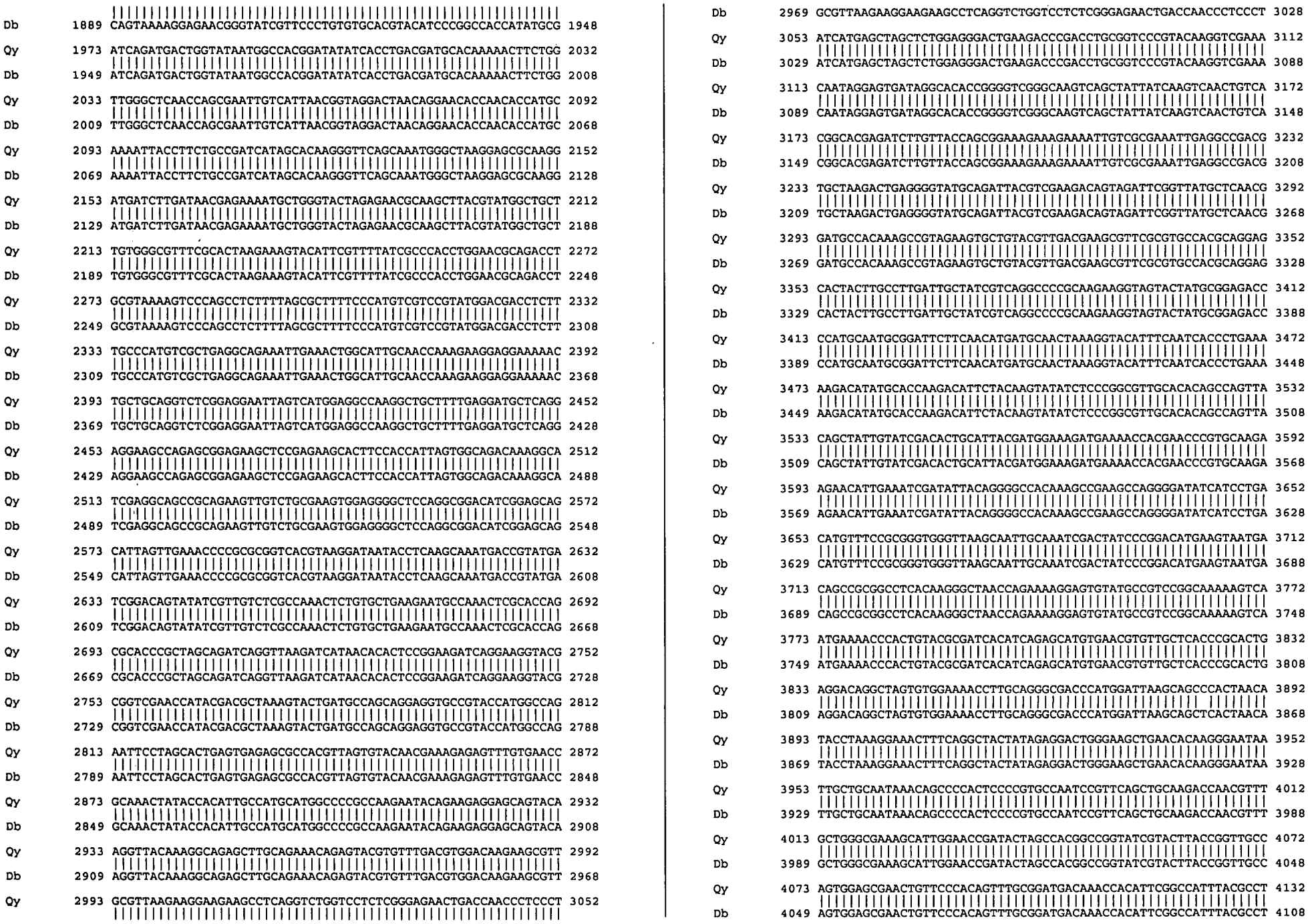
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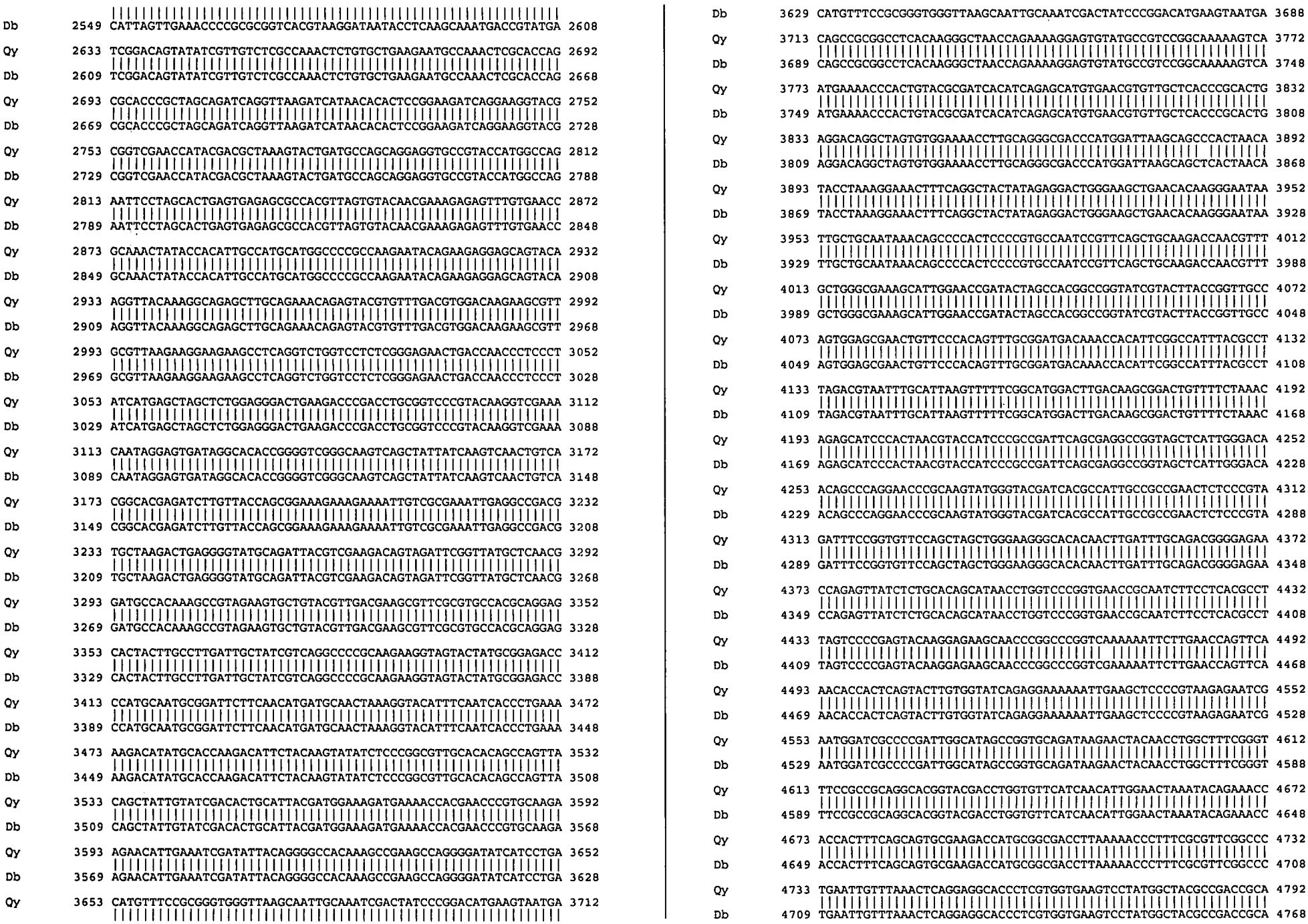
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Db 4529 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4588
Qy 4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
Db 4589 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4648
Qy 4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
Db 4649 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4708
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Qy      4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
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Qy      5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
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Qy      5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
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Qy      6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
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Qy      6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
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Qy      6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
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DEFINITION  Sequence 22 from Patent WO2004018506.
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VERSION     CQ790449.1  GI:45823491
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ivanova,L., Renner,W.A. and Saudan,P.
  TITLE     Inducible alphaviral/orip based gene expression system
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ORIGIN

  Query Match             89.7%;  Score 7657.2;  DB 6;  Length 17753;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7642;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

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Db        869 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 928

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
Db        929 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 988

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
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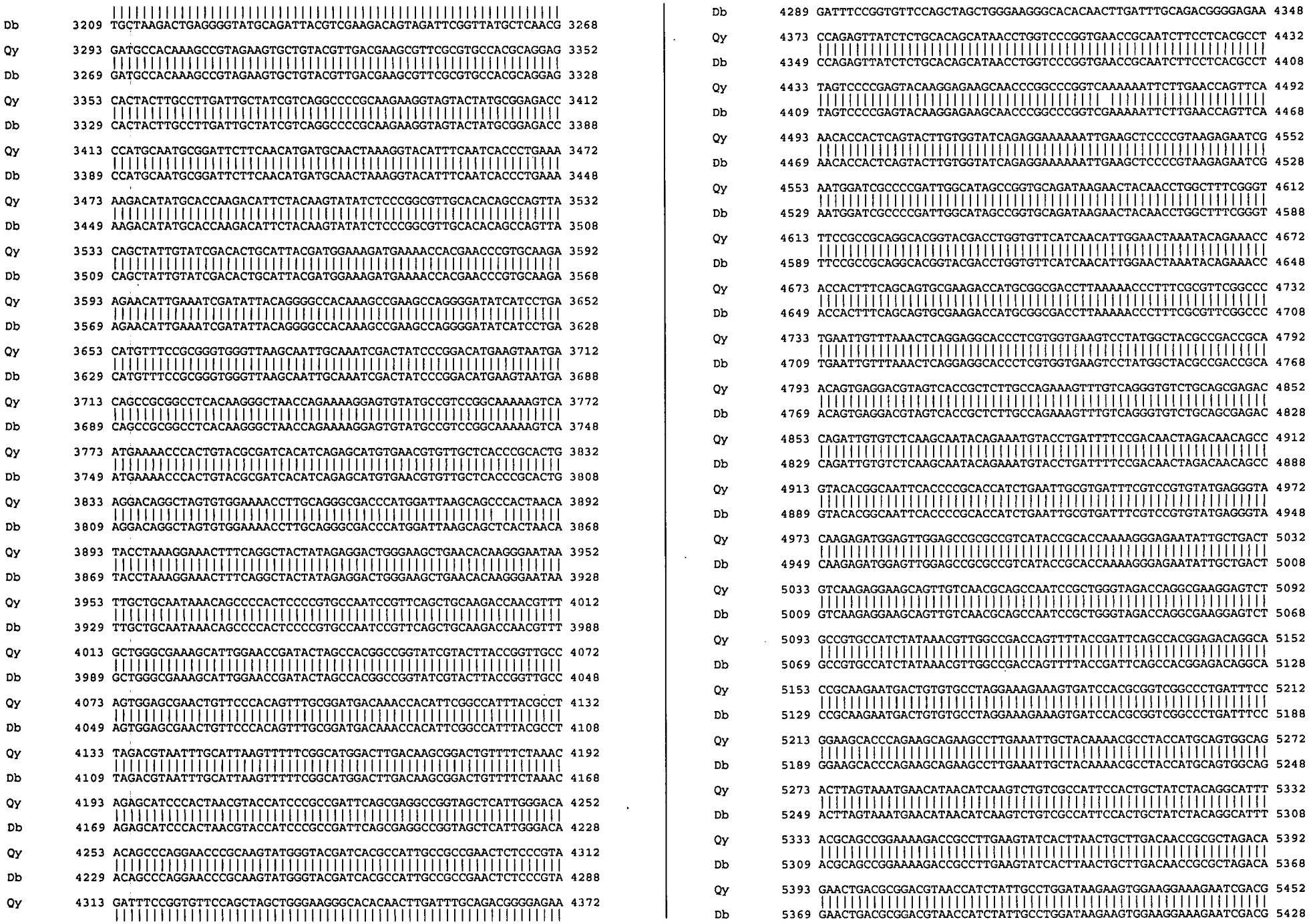
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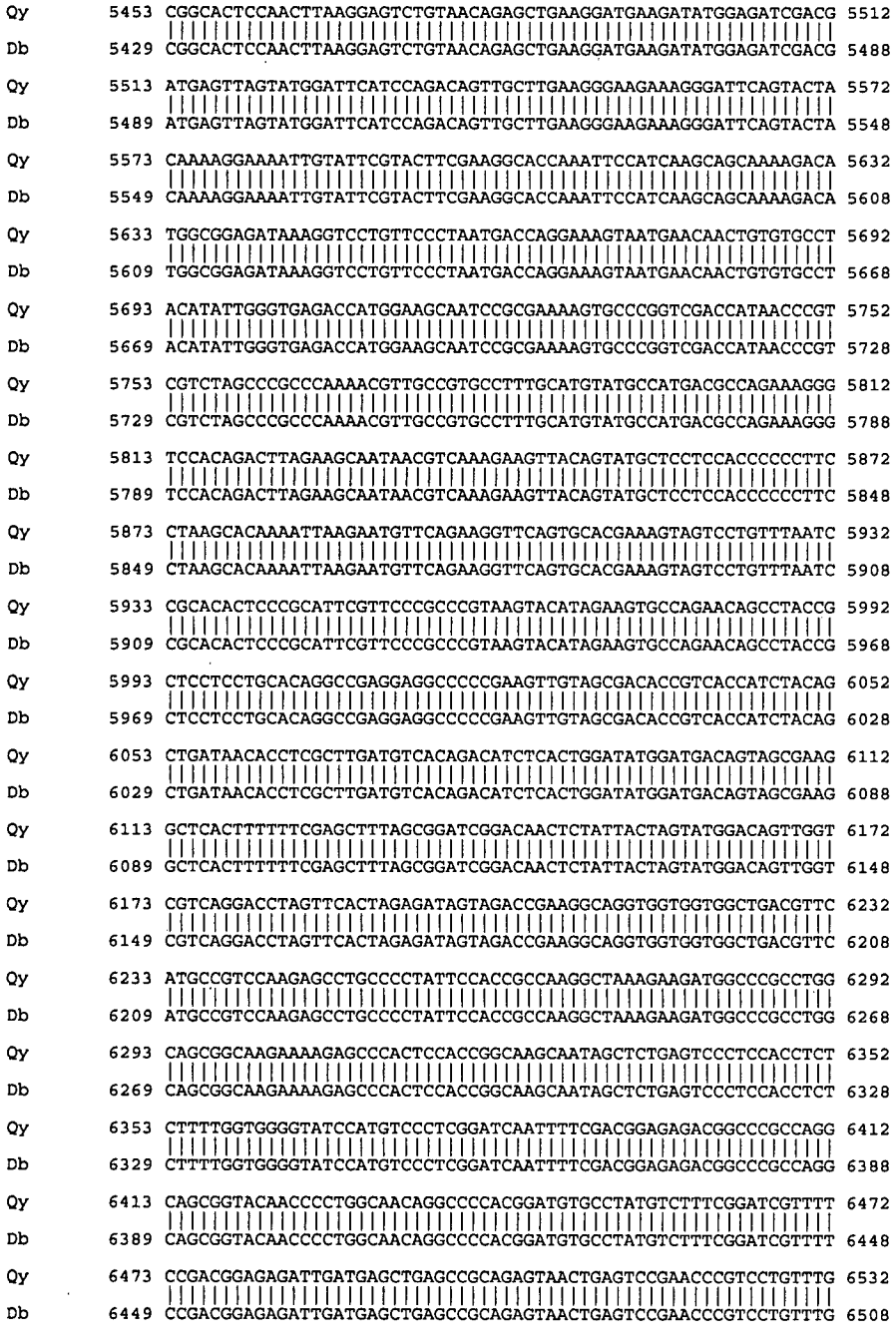
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RESULT 9
AR282858
LOCUS       AR282858               9951 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 3 from patent US 6524792.
ACCESSION   AR282858
VERSION     AR282858.1  GI:29719660
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 9951)
  AUTHORS   Renner,W.A., Orberger,G.H., Koller,D. and Bailey,J.E.
  TITLE     Expression cloning processes for the discovery, characterization
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  JOURNAL   Patent: US 6524792-A 3 25-FEB-2003;
FEATURES             Location/Qualifiers
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ORIGIN

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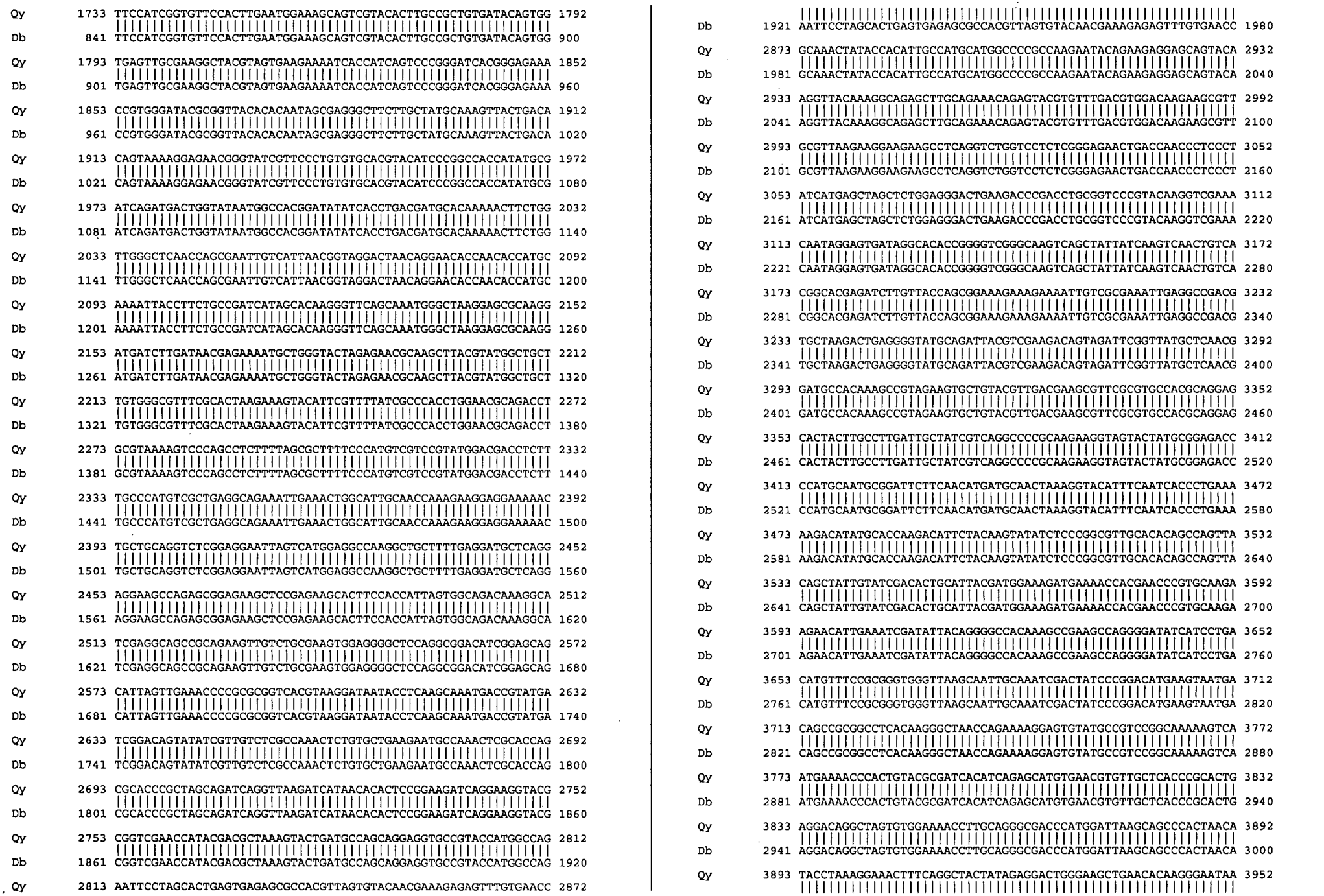
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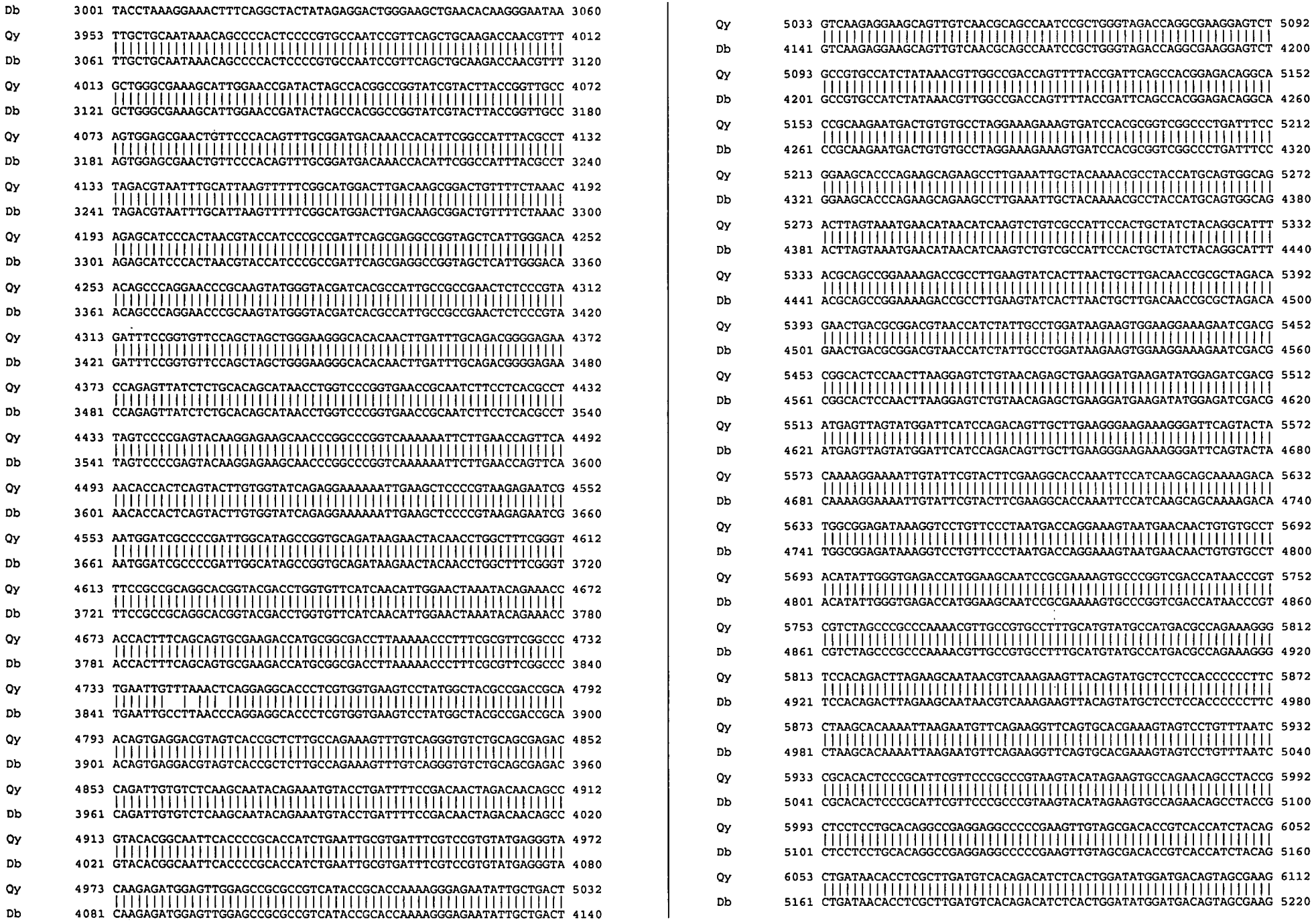
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Qy       6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
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Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
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Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
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Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
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Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
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Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
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Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
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Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
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Db       7321 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 7380

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RESULT 10
AX128602
LOCUS       AX128602                9951 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 2 from Patent WO0130989.
ACCESSION   AX128602
VERSION     AX128602.1  GI:14135064
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Renner,W.A. and Nieba,L.
  TITLE     Method for creating divergent populations of nucleic acid molecules
            and proteins
  JOURNAL   Patent: WO 0130989-A 2 03-MAY-2001;
            Cytos Biotechnology AG (CH) ; Renner, Wolfgand Andreas (CH) ;
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ORIGIN

  Query Match             89.4%;  Score 7637.4;  DB 6;  Length 9951;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7641;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
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Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
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Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
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Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
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Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
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Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
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Db        1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320

Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
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Db        1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380

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Db      1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560

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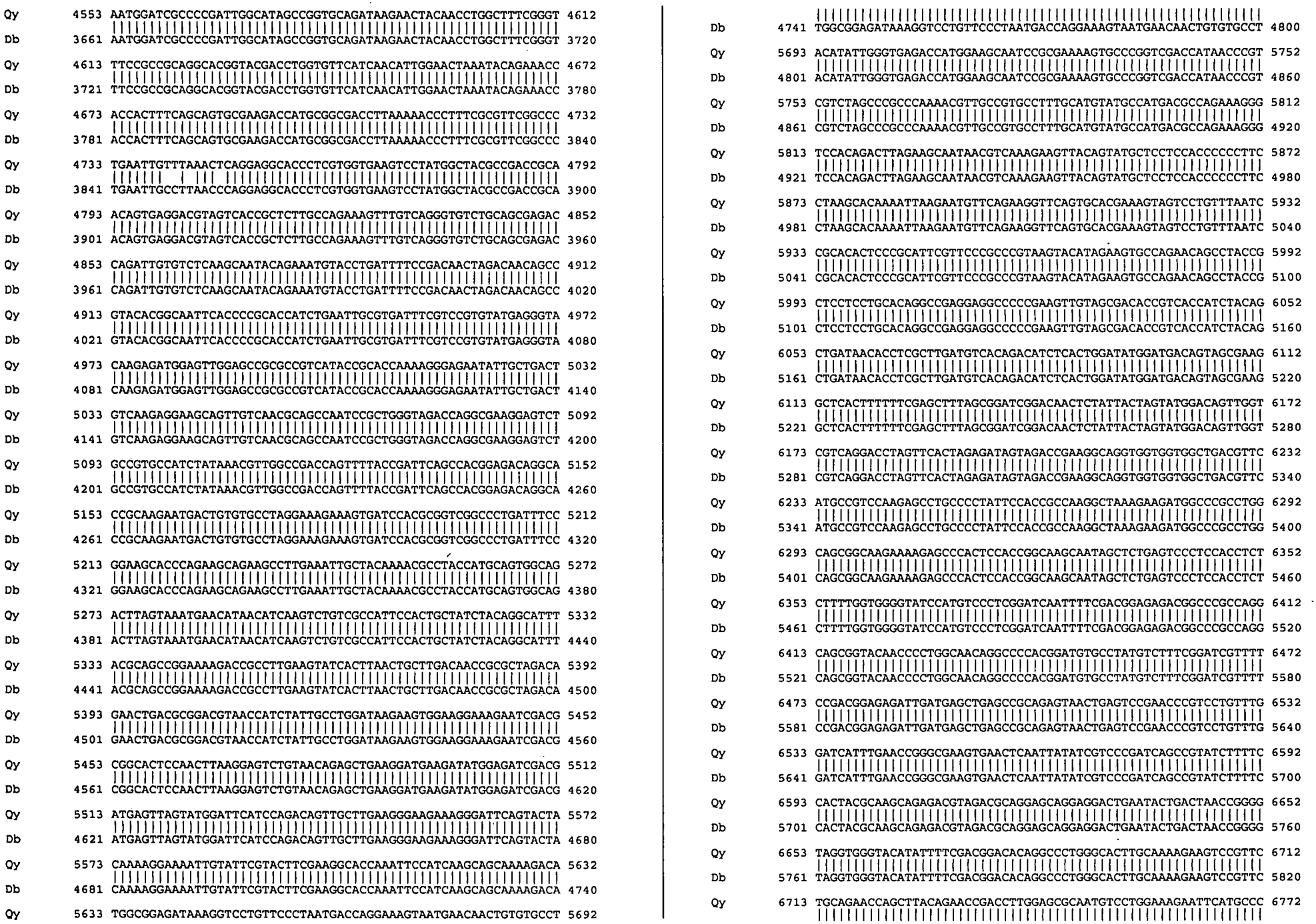

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ACCESSION   AR282859
VERSION     AR282859.1  GI:29719661
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10524)
  AUTHORS   Renner,W.A., Orberger,G.H., Koller,D. and Bailey,J.E.
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ORIGIN

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Qy      3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
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Qy      3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
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Qy      3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
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Qy      3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
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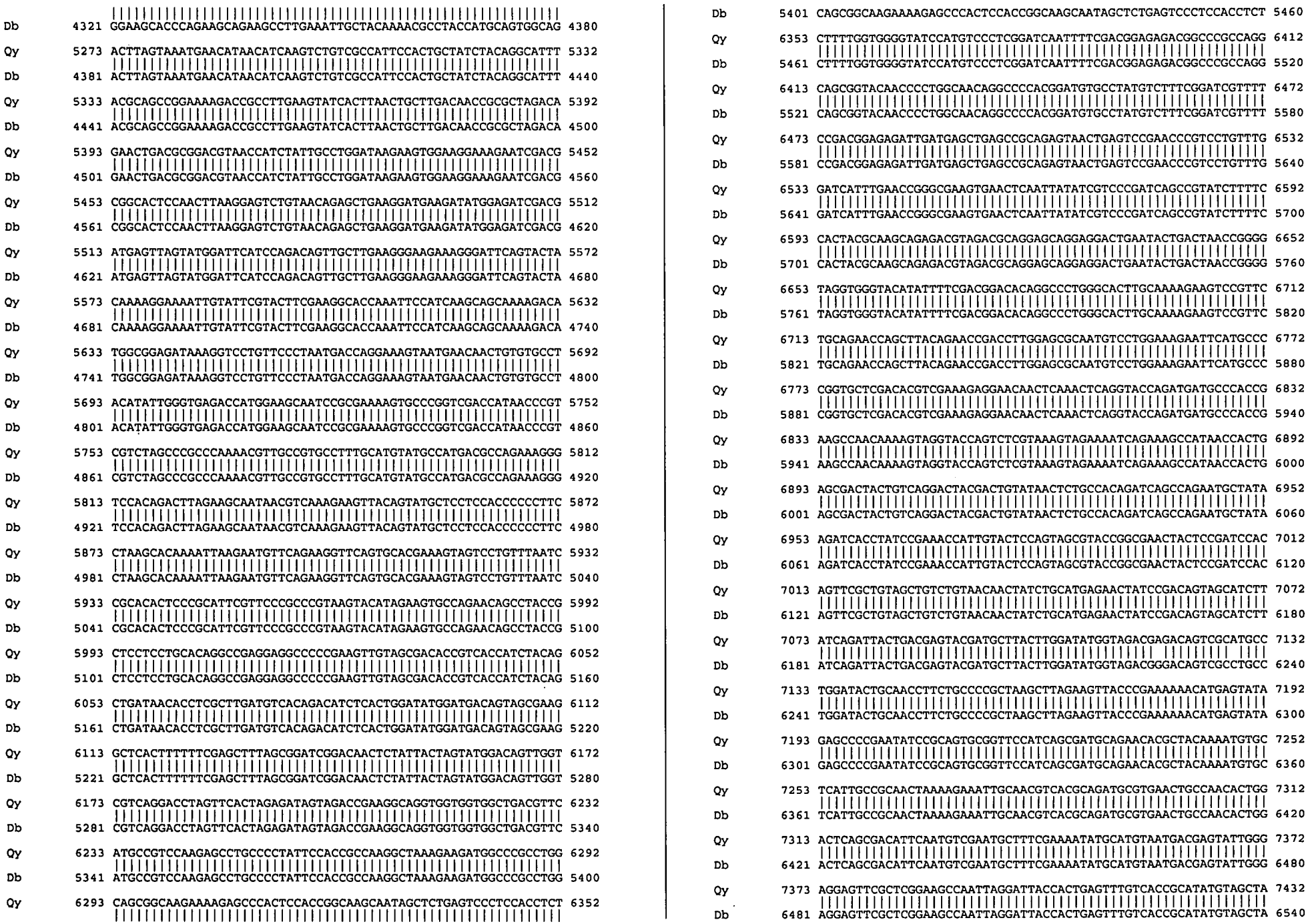
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RESULT 12
AR282860
LOCUS AR282860 11927 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 5 from patent US 6524792.
ACCESSION AR282860
VERSION AR282860.1 GI:29719662
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 11927)
AUTHORS Renner,W.A., Orberger,G.H., Koller,D. and Bailey,J.E.
TITLE Expression cloning processes for the discovery, characterization and isolation of genes encoding polypeptides with a predetermined property
JOURNAL Patent: US 6524792-A 5 25-FEB-2003;
FEATURES Location/Qualifiers
source 1. .11927
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 89.4%; Score 7637.4; DB 6; Length 11927;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
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Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
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Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
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Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

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Qy       3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
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Db      3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540

Qy      4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
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Qy      4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
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Db       5341 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 5400
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Qy       6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
Db       5461 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 5520
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Qy       6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
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Db       5761 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 5820
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Db       5821 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 5880
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Db       6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540
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Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
Db       6721 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 6780
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Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
Db       7081 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 7140
Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
Db       7141 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 7200
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Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
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Db       7201 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 7260

Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
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Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
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Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
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Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
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Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
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Db       7621 CTGACTAATACTACAACACCACCACCT 7647


RESULT 13
AR137241
LOCUS       AR137241               13905 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 1 from patent US 6197502.
ACCESSION   AR137241
VERSION     AR137241.1  GI:14478750
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13905)
  AUTHORS   Renner,W.A., Orberger,G.H., Koller,D. and Bailey,J.E.
  TITLE     Expression cloning processes for the discovery characterization,
            and isolation of genes encoding polypeptides with a predetermined
            property
  JOURNAL   Patent: US 6197502-A 1 06-MAR-2001;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             89.4%;  Score 7637.4;  DB 6;  Length 13905;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7641;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
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Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
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Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
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Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
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Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
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Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
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Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
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Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
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Db        901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
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Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
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Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
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Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
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Db        1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260

Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
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Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
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Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
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Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700

Qy       3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 2760

Qy       3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820

Qy       3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880

Qy       3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940

Qy       3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3000

Qy       3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060

Qy       3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120

Qy       4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
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Db       3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180

Qy       4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240

Qy       4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 3300

Qy       4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360

Qy       4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
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Db       3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420

Qy       4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480

Qy       4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
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Db       3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660
Qy       4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
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Db       3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780
Qy       4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
Db       3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840
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Qy       4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
Db       3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960
Qy       4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
Db       3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020
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Db       4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080
Qy       4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
Db       4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140
Qy       5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
Db       4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200
Qy       5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
Db       4201 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 4260
Qy       5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
Db       4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320
Qy       5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
Db       4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380
Qy       5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
Db       4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440
Qy       5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
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Qy       5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
Db       4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620
Qy       5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
Db       4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680
Qy       5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
Db       4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740
Qy       5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
Db       4741 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 4800
Qy       5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
Db       4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860
Qy       5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
Db       4861 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 4920
Qy       5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
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Qy       5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
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Qy       5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
Db       5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100
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Qy       6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
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Qy       6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
Db       5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340
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Qy       6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
Db       5401 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 5460
Qy       6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
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Qy       6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
Db       5521 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 5580
Qy       6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
Db       5581 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 5640
Qy       6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
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Qy       6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
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Db       5701 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 5760

Qy       6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
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Db       5761 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 5820

Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
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Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 5940

Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
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Db       5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000

Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6060

Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
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Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
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Db       6121 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 6180

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Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
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Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
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Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
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Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
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Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
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Db       7321 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 7380

Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
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Db       7381 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 7440

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
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Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
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Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
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Db       7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 7620

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RESULT 14
AR282856
LOCUS       AR282856               13905 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 1 from patent US 6524792.
ACCESSION   AR282856
VERSION     AR282856.1  GI:29719658
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13905)
  AUTHORS   Renner,W.A., Orberger,G.H., Koller,D. and Bailey,J.E.
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  TITLE     Expression cloning processes for the discovery, characterization
            and isolation of genes encoding polypeptides with a predetermined
            property
  JOURNAL   Patent: US 6524792-A 1 25-FEB-2003;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             89.4%;  Score 7637.4;  DB 6;  Length 13905;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7641;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
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Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140

Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 1200

Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260

Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320

Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380

Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440

Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500

Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560

Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620

Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680

Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740

Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1741 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 1800

Qy       2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1801 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 1860

Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1861 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 1920

Qy       2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980
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Qy    2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2040

Qy    2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100

Qy    2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 2160

Qy    3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 2220

Qy    3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280

Qy    3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340

Qy    3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400

Qy    3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 2460

Qy    3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 2520

Qy    3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 2580

Qy    3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 2640

Qy    3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700

Qy    3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 2760

Qy    3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820

Qy    3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880

Qy    3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940

Qy    3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3000

Qy    3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060

Qy    3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120

Qy    4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180

Qy    4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240

Qy    4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 3300

Qy    4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360

Qy    4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420

Qy    4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480

Qy    4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540

Qy    4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3541 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 3600

Qy    4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660

Qy    4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3661 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 3720

Qy    4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780

Qy    4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840

Qy    4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
           |||||||  | |||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900

Qy    4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960

Qy    4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020

Qy    4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080

Qy    4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140

Qy    5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200

Qy       5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 4260

Qy       5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320

Qy       5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380

Qy       5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440

Qy       5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 4500

Qy       5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560

Qy       5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620

Qy       5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680

Qy       5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
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Db       4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740

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Qy       5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
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Qy       5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
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RESULT 15
AR221249
LOCUS AR221249 8000 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 102 from patent US 6426196.
ACCESSION AR221249
VERSION AR221249.1 GI:23328145
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 8000)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Schlesinger,S. and Frolov,I.
TITLE Alphavirus structural protein expression cassettes
JOURNAL Patent: US 6426196-A 102 30-JUL-2002;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 89.4%; Score 7634.8; DB 6; Length 8000;
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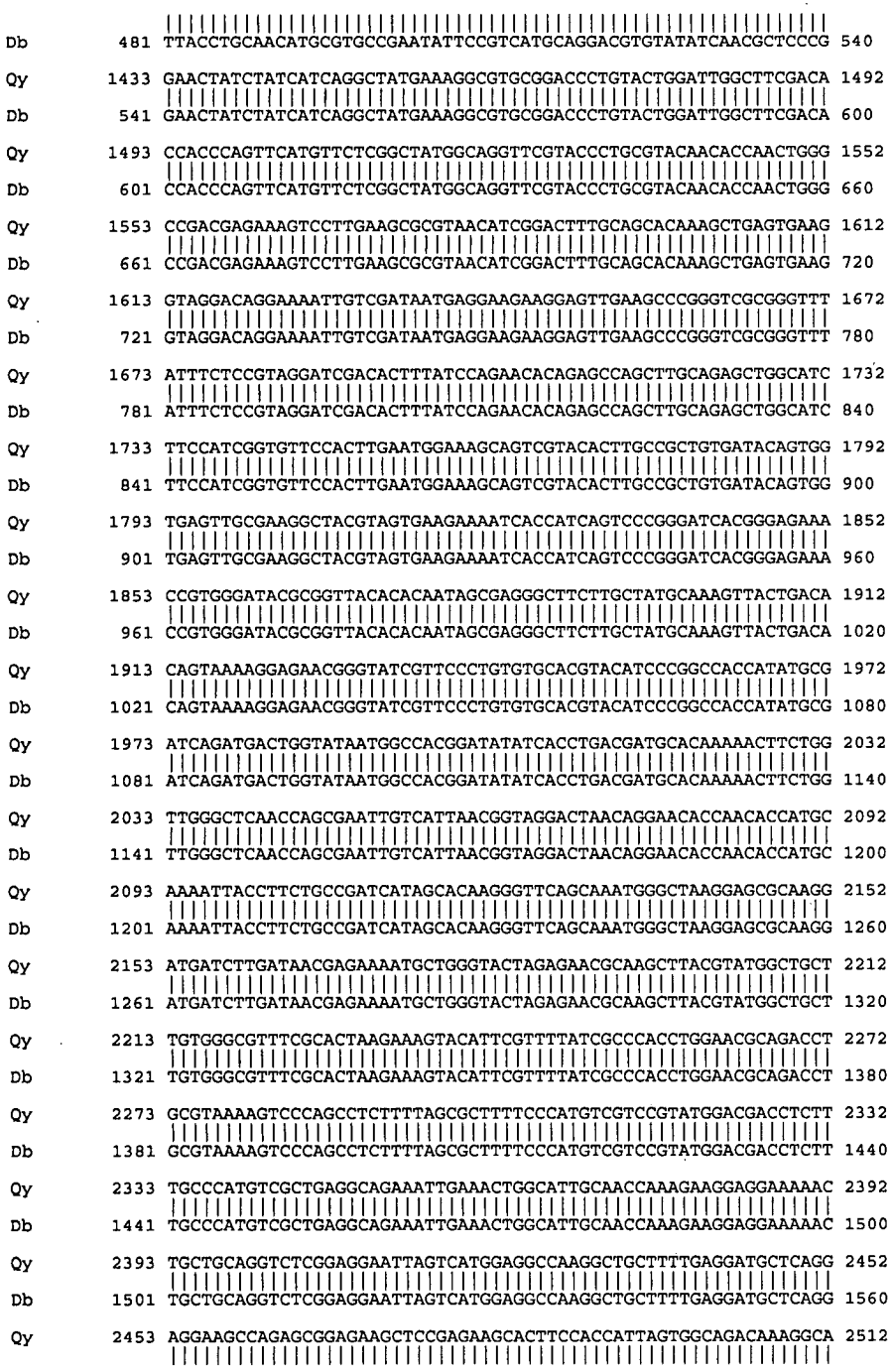
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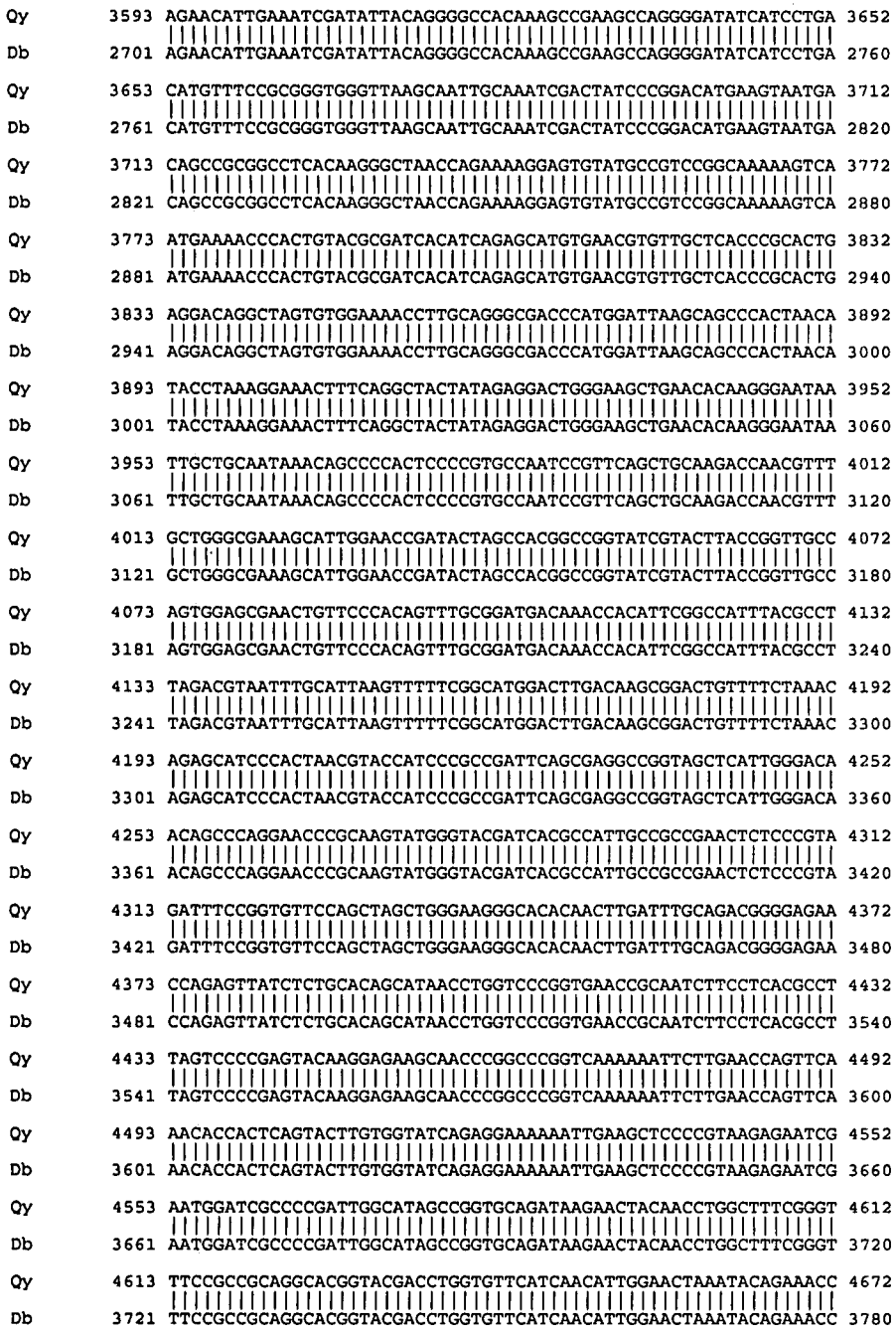
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Job time : 23457 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 08:17:54 ; Search time 16275 Seconds
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Searched: 34239544 seqs, 19032134700 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_htc:*
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6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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c 2	616.8	7.2	860	7	CV089193	CV089193 est_c_vir
c 3	616.8	7.2	862	7	CN385663	CN385663 LE2TR04D1
c 4	616.8	7.2	874	7	CN385637	CN385637 LE2TR04C0
c 5	616.8	7.2	884	7	CN385877	CN385877 LE2TR04M1
c 6	616.8	7.2	899	7	CN385574	CN385574 LE2TR03P1
c 7	616.8	7.2	921	7	CN384456	CN384456 LE2TR01A0
c 8	608.8	7.1	805	2	BE421195	BE421195 HWM006.G0
c 9	607.8	7.1	685	5	BU724260	BU724260 SJMBFC05
c 10	607.8	7.1	702	6	CB549906	CB549906 MMPL0007_
c 11	607.8	7.1	714	6	CB548528	CB548528 MMPL0022_
c 12	607.8	7.1	753	5	BQ157858	BQ157858 NF103A09P
c 13	607.8	7.1	758	5	BQ158943	BQ158943 NF095D07P
c 14	607.8	7.1	764	5	BQ158750	BQ158750 NF070F07P
c 15	607.8	7.1	771	5	BQ158875	BQ158875 NF076G06P
c 16	607.8	7.1	773	5	BQ156760	BQ156760 NF096H04I
c 17	607.8	7.1	774	5	BQ158974	BQ158974 NF098A06P
c 18	607.8	7.1	775	5	BQ158844	BQ158844 NF073D03P
c 19	607.8	7.1	776	5	BQ159296	BQ159296 NF092H12P
c 20	607.8	7.1	779	5	BQ158936	BQ158936 NF083H10P
c 21	607.8	7.1	782	5	BQ158981	BQ158981 NF099E10P
c 22	607.8	7.1	794	5	BQ158923	BQ158923 NF083A12P
c 23	607.8	7.1	795	5	BQ157846	BQ157846 NF098C12P
c 24	607.8	7.1	799	1	AV405326	AV405326 AV405326
c 25	607.8	7.1	810	7	CV478551	CV478551 Lu6B6 Fla
c 26	607.8	7.1	815	7	CV478075	CV478075 Lu1A6 Fla
c 27	606.8	7.1	757	5	BQ158987	BQ158987 NF100G10P
c 28	606.8	7.1	758	5	BQ159010	BQ159010 NF102E04P
c 29	606.8	7.1	762	5	BQ158850	BQ158850 NF073H10P
c 30	606.8	7.1	768	5	BQ158329	BQ158329 NF047G06P
c 31	606.8	7.1	769	5	BQ159407	BQ159407 NF120B04P
c 32	606.8	7.1	770	5	BQ158852	BQ158852 NF074B11P
c 33	606.8	7.1	771	5	BQ158940	BQ158940 NF095A10P
c 34	606.8	7.1	776	5	BQ158753	BQ158753 NF071A06P
c 35	606.8	7.1	777	5	BQ159021	BQ159021 NF103G05P
c 36	606.8	7.1	779	5	BQ159399	BQ159399 NF118A11P
c 37	606.8	7.1	781	5	BQ158877	BQ158877 NF076G10P
c 38	606.8	7.1	781	5	BQ159263	BQ159263 NF090H06P
c 39	606.8	7.1	782	5	BQ158858	BQ158858 NF075C06P
c 40	606.8	7.1	784	5	BQ158848	BQ158848 NF074A07P
c 41	606.8	7.1	784	5	BQ158973	BQ158973 NF098A03P
c 42	606.8	7.1	786	5	BQ159035	BQ159035 NF104H08P
c 43	606.8	7.1	788	5	BQ158195	BQ158195 NF031B09P
c 44	606.8	7.1	792	5	BQ158756	BQ158756 NF071E09P
c 45	606.8	7.1	799	5	BQ158971	BQ158971 NF097D10P

ALIGNMENTS

RESULT 1
CN385673/c
LOCUS CN385673 813 bp mRNA linear EST 31-AUG-2004
DEFINITION LE2TR04D22 Tomato CL5915 roots under different developmental stages
Lycopersicon esculentum cDNA clone LE2TR04D22, mRNA sequence.
ACCESSION CN385673
VERSION CN385673.1 GI:51700987
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 813)
AUTHORS Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
TITLE DNA microarray profiling of gene expression during tomato root development
JOURNAL Unpublished (2004)
COMMENT Contact: Kin-Ying, To
Crop Plant Improvement Group
Institute of BioAgricultural Sciences, Academia Sinica
128 Academia Rd. Section 2, Taipei, Taiwan 11529
Tel: 886-2-2653-3161
Fax: 886-2-2561-5600
Email: kyto@gate.sinica.edu.tw
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Plate: 04 row: D column: 22
Seq primer: smart2.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/cultivar="CL5915"
/db_xref="taxon:4081"
/clone="LE2TR04D22"
/tissue_type="roots"
/dev_stage="1-,2-,3-, and 4- month-old"
/lab_host="E.coli BM25.8"
/clone_lib="Tomato CL5915 roots under different developmental stages"
/note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained from AVRDC.Roots were harvested from plants grown under different developmental stages: 1-,2-,3-,4-month-old. Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart PCR cDNA Library construction kit, Clontech)"
ORIGIN

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  Query Match             7.2%;  Score 616.8;  DB 7;  Length 813;
  Best Local Similarity   97.4%;  Pred. No. 1.5e-174;
  Matches  627;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          3 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 62
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Db        699 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 640

Qy         63 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 122
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Db        639 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 580

Qy        123 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 182
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Db        579 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 520

Qy        183 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 460

Qy        243 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 302
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Db        459 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 400

Qy        303 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 362
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Db        399 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 340

Qy        363 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 422
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Db        339 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 280

Qy        423 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 482
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Db        279 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 220

Qy        483 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
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Db        219 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 160

Qy        543 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 602
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Db        159 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 100

Qy        603 AAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
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Db         99 AAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 56
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RESULT 2
CV089193/c
LOCUS       CV089193                860 bp    mRNA    linear   EST 26-AUG-2004
DEFINITION  est_c_virginica2856 Cv Hepatopancreas Crassostrea virginica cDNA,
            mRNA sequence.
ACCESSION   CV089193
VERSION     CV089193.1  GI:51568542
KEYWORDS    EST.
SOURCE      Crassostrea virginica (eastern oyster)
  ORGANISM  Crassostrea virginica
            Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Ostreoida;
            Ostreoidea; Ostreidae; Crassostrea.
REFERENCE   1  (bases 1 to 860)
  AUTHORS   Jenny,M.J., Warr,G.W., Gross,P.S., Almeida,J.S., Chen,Y.,
            McKillen,D.J., Wu,S. and Chapman,R.W.
  TITLE     Crassostrea virginica EST Library at marinegenomics.org
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Gross PS
            Department of Biochemistry and Molecular Biology
            Medical University of South Carolina
            Box 250509, 173 Ashley Avenue, Charleston, SC 29425, USA
            Tel: 846 792 8503
            Fax: 843 792 4850
            Email: grossp@musc.edu.
FEATURES             Location/Qualifiers
     source          1. .860
                     /organism="Crassostrea virginica"
                     /mol_type="mRNA"
                     /db_xref="taxon:6565"
                     /cell_type="hepatopancreas"
                     /clone_lib="Cv Hepatopancreas"
                     /note="Vector: pTriplEx2; Site_1: Sfi I; Site_2: Sfi I"
ORIGIN
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  Query Match             7.2%;  Score 616.8;  DB 7;  Length 860;
  Best Local Similarity   97.4%;  Pred. No. 1.6e-174;
  Matches  627;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          3 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 62
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Db        707 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 648

Qy         63 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 122
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Db        647 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 588

Qy        123 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 528

Qy        183 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 242
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Db        527 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 468

Qy        243 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 408

Qy        303 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 362
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Db        407 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 348

Qy        363 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 422
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Db        347 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 288

Qy        423 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 228

Qy        483 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 168

Qy        543 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 108

Qy        603 AAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
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Db        107 AAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 64
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RESULT 3
CN385663/c
LOCUS       CN385663                862 bp    mRNA    linear   EST 31-AUG-2004
DEFINITION  LE2TR04D12 Tomato CL5915 roots under different developmental stages
            Lycopersicon esculentum cDNA clone LE2TR04D12, mRNA sequence.
ACCESSION   CN385663
VERSION     CN385663.1  GI:51700977
KEYWORDS    EST.
SOURCE      Lycopersicon esculentum (tomato)
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
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REFERENCE   1  (bases 1 to 862)
  AUTHORS   Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
  TITLE     DNA microarray profiling of gene expression during tomato root
            development
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Kin-Ying, To
            Crop Plant Improvement Group
            Institute of BioAgricultural Sciences, Academia Sinica
            128 Academia Rd. Section 2, Taipei, Taiwan 11529
            Tel: 886-2-2653-3161
            Fax: 886-2-2561-5600
            Email: kyto@gate.sinica.edu.tw
            Insert Length: 862   Std Error: 0.00
            Plate: 04  row: D  column: 12
            Seq primer: smart2.
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                     /clone="LE2TR04D12"
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                     /dev_stage="1-,2-,3-, and 4- month-old"
                     /lab_host="E.coli BM25.8"
                     /clone_lib="Tomato CL5915 roots under different
                     developmental stages"
                     /note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained
                     from AVRDC.Roots were harvested from plants grown under
                     different developmental stages: 1-,2-,3-,4-month-old.
                     Equal aliquots of mRNA of different developmental stages
                     were mixed and used for cDNA library construction. (Smart
                     PCR cDNA Library construction kit, Clontech)"
ORIGIN

  Query Match             7.2%;  Score 616.8;  DB 7;  Length 862;
  Best Local Similarity   97.4%;  Pred. No. 1.6e-174;
  Matches  627;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          3 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 62
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Db        699 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 640

Qy         63 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 122
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Db        639 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 580

Qy        123 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 182
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Db        579 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 520

Qy        183 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 460

Qy        243 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 400

Qy        303 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 362
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Db        399 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 340

Qy        363 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 422
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Db        339 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 280

Qy        423 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 482
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Db        279 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 220

Qy        483 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
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Db        219 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 160

Qy        543 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 602
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Qy        603 AAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
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Db         99 AAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 56


RESULT 4
CN385637/c
LOCUS       CN385637                874 bp    mRNA    linear   EST 31-AUG-2004
DEFINITION  LE2TR04C09 Tomato CL5915 roots under different developmental stages
            Lycopersicon esculentum cDNA clone LE2TR04C09, mRNA sequence.
ACCESSION   CN385637
VERSION     CN385637.1  GI:51700951
KEYWORDS    EST.
SOURCE      Lycopersicon esculentum (tomato)
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE   1  (bases 1 to 874)
  AUTHORS   Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
  TITLE     DNA microarray profiling of gene expression during tomato root
            development
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Kin-Ying, To
            Crop Plant Improvement Group
            Institute of BioAgricultural Sciences, Academia Sinica
            128 Academia Rd. Section 2, Taipei, Taiwan 11529
            Tel: 886-2-2653-3161
            Fax: 886-2-2561-5600
            Email: kyto@gate.sinica.edu.tw
            Insert Length: 874   Std Error: 0.00
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FEATURES             Location/Qualifiers
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                     /tissue_type="roots"
                     /dev_stage="1-,2-,3-, and 4- month-old"
                     /lab_host="E.coli BM25.8"
                     /clone_lib="Tomato CL5915 roots under different
                     developmental stages"
                     /note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained
                     from AVRDC.Roots were harvested from plants grown under
                     different developmental stages: 1-,2-,3-,4-month-old.
                     Equal aliquots of mRNA of different developmental stages
                     were mixed and used for cDNA library construction. (Smart
                     PCR cDNA Library construction kit, Clontech)"
ORIGIN

  Query Match             7.2%;  Score 616.8;  DB 7;  Length 874;
  Best Local Similarity   97.4%;  Pred. No. 1.6e-174;
  Matches  627;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          3 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 640

Qy         63 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 122
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Db        639 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 580

Qy        123 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 182
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Db        579 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 520

Qy        183 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 242
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Db        519 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 460

Qy        243 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 302
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Db        459 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 400

Qy        303 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 340

Qy        363 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 422
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Db        339 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 280

Qy        423 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 482
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Db        279 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 220

Qy        483 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 160

Qy        543 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 100

Qy        603 AAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
              |||||||||||||||    |   || | |  ||  | |||
Db         99 AAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 56
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RESULT 5
CN385877/c
LOCUS CN385877 884 bp mRNA linear EST 31-AUG-2004
DEFINITION LE2TR04M16 Tomato CL5915 roots under different developmental stages
Lycopersicon esculentum cDNA clone LE2TR04M16, mRNA sequence.
ACCESSION CN385877
VERSION CN385877.1 GI:51701191
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 884)
AUTHORS Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
TITLE DNA microarray profiling of gene expression during tomato root development
JOURNAL Unpublished (2004)
COMMENT Contact: Kin-Ying, To
Crop Plant Improvement Group
Institute of BioAgricultural Sciences, Academia Sinica
128 Academia Rd. Section 2, Taipei, Taiwan 11529
Tel: 886-2-2653-3161
Fax: 886-2-2561-5600
Email: kyto@gate.sinica.edu.tw
Insert Length: 884 Std Error: 0.00
Plate: 04 row: M column: 16
Seq primer: smart2.
FEATURES Location/Qualifiers
source 1. .884
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="CL5915"
/db_xref="taxon:4081"
/clone="LE2TR04M16"
/tissue_type="roots"
/dev_stage="1-,2-,3-, and 4- month-old"
/lab_host="E.coli BM25.8"
/clone_lib="Tomato CL5915 roots under different developmental stages"
/note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained from AVRDC.Roots were harvested from plants grown under different developmental stages: 1-,2-,3-,4-month-old. Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart PCR cDNA Library construction kit, Clontech)"
ORIGIN

Query Match 7.2%; Score 616.8; DB 7; Length 884;
Best Local Similarity 97.4%; Pred. No. 1.6e-174;
Matches 627; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Qy          3 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 640

Qy         63 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 580

Qy        123 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 520

Qy        183 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 460

Qy        243 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 400

Qy        303 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 340

Qy        363 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 280

Qy        423 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 220

Qy        483 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 160

Qy        543 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 100

Qy        603 AAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
              |||||||||||||||    |   || | |  ||  | |||
Db         99 AAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 56
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RESULT 6
CN385574/c
LOCUS CN385574 899 bp mRNA linear EST 31-AUG-2004
DEFINITION LE2TR03P18 Tomato CL5915 roots under different developmental stages
Lycopersicon esculentum cDNA clone LE2TR03P18, mRNA sequence.
ACCESSION CN385574
VERSION CN385574.1 GI:51700888
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 899)

```
  AUTHORS   Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
  TITLE     DNA microarray profiling of gene expression during tomato root
            development
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Kin-Ying, To
            Crop Plant Improvement Group
            Institute of BioAgricultural Sciences, Academia Sinica
            128 Academia Rd. Section 2, Taipei, Taiwan 11529
            Tel: 886-2-2653-3161
            Fax: 886-2-2561-5600
            Email: kyto@gate.sinica.edu.tw
            Insert Length: 899   Std Error: 0.00
            Plate: 03  row: P  column: 18
            Seq primer: smart2.
FEATURES             Location/Qualifiers
     source          1. .899
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                     /mol_type="mRNA"
                     /cultivar="CL5915"
                     /db_xref="taxon:4081"
                     /clone="LE2TR03P18"
                     /tissue_type="roots"
                     /dev_stage="1-,2-,3-, and 4- month-old"
                     /lab_host="E.coli BM25.8"
                     /clone_lib="Tomato CL5915 roots under different
                     developmental stages"
                     /note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained
                     from AVRDC.Roots were harvested from plants grown under
                     different developmental stages: 1-,2-,3-,4-month-old.
                     Equal aliquots of mRNA of different developmental stages
                     were mixed and used for cDNA library construction. (Smart
                     PCR cDNA Library construction kit, Clontech)"
ORIGIN

  Query Match             7.2%;  Score 616.8;  DB 7;  Length 899;
  Best Local Similarity   97.4%;  Pred. No. 1.6e-174;
  Matches  627;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          3 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 640

Qy         63 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 580

Qy        123 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 520

Qy        183 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 460

Qy        243 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 400

Qy        303 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 340

Qy        363 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 280

Qy        423 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 220

Qy        483 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 160

Qy        543 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 100

Qy        603 AAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
              |||||||||||||||     |    || | |  ||  | |||
Db         99 AAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 56


RESULT 7
CN384456/c
LOCUS       CN384456                921 bp    mRNA    linear   EST 31-AUG-2004
DEFINITION  LE2TR01A01 Tomato CL5915 roots under different developmental stages
            Lycopersicon esculentum cDNA clone LE2TR01A01, mRNA sequence.
ACCESSION   CN384456
VERSION     CN384456.1  GI:51699770
KEYWORDS    EST.
SOURCE      Lycopersicon esculentum (tomato)
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
  TITLE     DNA microarray profiling of gene expression during tomato root
            development
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Kin-Ying, To
            Crop Plant Improvement Group
            Institute of BioAgricultural Sciences, Academia Sinica
            128 Academia Rd. Section 2, Taipei, Taiwan 11529
            Tel: 886-2-2653-3161
            Fax: 886-2-2561-5600
            Email: kyto@gate.sinica.edu.tw
            Insert Length: 921   Std Error: 0.00
            Plate: 01  row: A  column: 01
            Seq primer: smart2.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="CL5915"
                     /db_xref="taxon:4081"
                     /clone="LE2TR01A01"
                     /tissue_type="roots"
                     /dev_stage="1-,2-,3-, and 4- month-old"
                     /lab_host="E.coli BM25.8"
                     /clone_lib="Tomato CL5915 roots under different
                     developmental stages"
                     /note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained
                     from AVRDC.Roots were harvested from plants grown under
                     different developmental stages: 1-,2-,3-,4-month-old.
                     Equal aliquots of mRNA of different developmental stages
                     were mixed and used for cDNA library construction. (Smart
                     PCR cDNA Library construction kit, Clontech)"
ORIGIN

  Query Match             7.2%;  Score 616.8;  DB 7;  Length 921;
  Best Local Similarity   97.4%;  Pred. No. 1.6e-174;
  Matches  627;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          3 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 640

Qy         63 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 580

Qy        123 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 520
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Qy        183 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 460

Qy        243 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 400

Qy        303 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 340

Qy        363 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 280

Qy        423 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 220

Qy        483 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 160

Qy        543 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 100

Qy        603 AAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
              ||||||||||||||||  |    || | |  ||  | |||
Db         99 AAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 56
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RESULT 8
BE421195/c

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LOCUS       BE421195                 805 bp    mRNA    linear   EST 24-JUL-2000
DEFINITION  HWM006.G08 ITEC HWM Barley Leaf Library Hordeum vulgare subsp.
            vulgare cDNA clone HWM006.G08, mRNA sequence.
ACCESSION   BE421195
VERSION     BE421195.1  GI:9419038
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 805)
  AUTHORS   Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T.,
            Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A.,
            Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J.,
            Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P.,
            Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G.,
            Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.
  TITLE     International Triticeae EST Cooperative (ITEC): Production of
            Expressed Sequence Tags for Species of the Triticeae
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Herrmann RG
            Botanisches Institut der LMU
            Menzinger Str. 67, D-80638 Munchen GERMANY
            Fax: 49 30 171683
            Email: herrmann@botanik.biologie.uni-muenchen.de
            International Triticeae EST Cooperative (ITEC)
            http://wheat.pw.usda.gov/genome.
FEATURES             Location/Qualifiers
     source          1. .805
                     /organism="Hordeum vulgare subsp. vulgare"
                     /mol_type="mRNA"
                     /cultivar="barke"
                     /sub_species="vulgare"
                     /db_xref="taxon:112509"
                     /clone="HWM006.G08"
                     /tissue_type="leaf"
                     /dev_stage="14 day old"
                     /clone_lib="ITEC HWM Barley Leaf Library"
                     /note="Vector: pBluescriptSK(-); 850 bp average insert
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ORIGIN
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  Query Match             7.1%;  Score 608.8;  DB 2;  Length 805;
  Best Local Similarity   99.4%;  Pred. No. 4.1e-172;
  Matches  621;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              |||||||| |||||||||||||||||| || ||||||||||||||||||||||||||||
Db        777 CTGACGCGGCCTGTAGCGGCGCATTAAGCNCGCCGGGTGTGGTGGTTACGCGCAGCGTGA 718

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        717 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 658

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 598

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 538

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 478

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 418

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTT-AAAAAATGAGCTGATTTAACAAAAA 419
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        417 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAAATGAGCTGATTTAACAAAAA 358

Qy        420 TTTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGC 479
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Db        357 TTTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGC 298

Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 238

Qy        540 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 178

Qy        600 GTAAAACGACGGCCAGTGAGCGCGC 624
              |||||||||||||||||||||||||
Db        177 GTAAAACGACGGCCAGTGAGCGCGC 153
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RESULT 9
BU724260/c

```
LOCUS       BU724260                 685 bp    mRNA    linear   EST 23-OCT-2003
DEFINITION  SJMBFC05 SJM Schistosoma japonicum cDNA similar to gb|AAB53629.1|
            (U84006) beta-galactosidase [Expression vector pBSII-LUCINT], mRNA
            sequence.
ACCESSION   BU724260
VERSION     BU724260.1  GI:28331629
KEYWORDS    EST.
SOURCE      Schistosoma japonicum
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 685)
  AUTHORS   Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R.,
            Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J.,
            Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
            McManus,D.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G.
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  TITLE     Evolutionary and biomedical implications of a Schistosoma japonicum
            complementary DNA resource
  JOURNAL   Nat. Genet. 35 (2), 139-147 (2003)
  MEDLINE   22879925
   PUBMED   12973349
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn.
FEATURES             Location/Qualifiers
     source          1. .685
                     /organism="Schistosoma japonicum"
                     /mol_type="mRNA"
                     /db_xref="taxon:6182"
                     /sex="male"
                     /tissue_type="Whole body"
                     /dev_stage="adult"
                     /lab_host="rabbits"
                     /clone_lib="SJM"
ORIGIN

  Query Match             7.1%;  Score 607.8;  DB 5;  Length 685;
  Best Local Similarity   97.2%;  Pred. No. 7.8e-172;
  Matches  629;  Conservative    0;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        675 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 616

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
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Db        615 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 556

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 496

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 436

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 376

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 316

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
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Db        315 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 256

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT-CCATTCGCCATTCAGGCTGC 479
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        255 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTGCCATTCGCCATTCAGGCTGC 196

Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
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Db        195 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 136

Qy        540 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 599
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Db        135 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 76

Qy        600 GTAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
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RESULT 10
CB549906/c
LOCUS       CB549906                 702 bp    mRNA    linear   EST 01-JUN-2003
DEFINITION  MMPL0007_B01 MMPL Macaca mulatta cDNA, mRNA sequence.
ACCESSION   CB549906
VERSION     CB549906.1  GI:31299101
KEYWORDS    EST.
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 702)
  AUTHORS   Katze,M.G., Bumgarner,R., Korth,M., Feldman,R., Amjadi,M. and
            Holzman,T.
  TITLE     Expressed sequence tags from Rhesus macaque placenta
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Holzman T
            Katze Lab
            University of Washington
            Box 358070, Seattle, WA 98195-8070, USA
            Tel: 206 732 6156
            Fax: 206 732 6055
            Email: ted@locke.hs.washington.edu
            Similar to GenBank entry HSU94592 U94592 Human uncoupling protein
            homolog (UCPH) mRNA, complete cds. 6/2002
            Plate: MMPL0007  row: B  column: 01.
FEATURES             Location/Qualifiers
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                     /organism="Macaca mulatta"
                     /mol_type="mRNA"
                     /db_xref="taxon:9544"
                     /sex="male"
                     /dev_stage="neonatal"
                     /clone_lib="MMPL"
                     /note="Organ: placenta"
ORIGIN

  Query Match             7.1%;  Score 607.8;  DB 6;  Length 702;
  Best Local Similarity   97.2%;  Pred. No. 7.9e-172;
  Matches  629;  Conservative    0;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 610

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 550

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 490

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 430

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 370

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 310

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 250

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT-CCATTCGCCATTCAGGCTGC 479
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Db        249 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTGCCATTCGCCATTCAGGCTGC 190
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Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 130

Qy        540 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 599
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Db        129 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 70

Qy        600 GTAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
              |||||||||||||||||||      |    || | |  ||  | |||
Db         69 GTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 23


RESULT 11
CB548528/c
LOCUS       CB548528                 714 bp    mRNA    linear   EST 01-JUN-2003
DEFINITION  MMPL0022_H09 MMPL Macaca mulatta cDNA, mRNA sequence.
ACCESSION   CB548528
VERSION     CB548528.1  GI:31297723
KEYWORDS    EST.
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 714)
  AUTHORS   Katze,M.G., Bumgarner,R., Korth,M., Peldman,R., Amjadi,M. and
            Holzman,T.
  TITLE     Expressed sequence tags from Rhesus macaque placenta
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Holzman T
            Katze Lab
            University of Washington
            Box 358070, Seattle, WA 98195-8070, USA
            Tel: 206 732 6156
            Fax: 206 732 6055
            Email: ted@locke.hs.washington.edu
            Similar to GenBank entry HSU94592 U94592 Human uncoupling protein
            homolog (UCPH) mRNA, complete cds. 6/2002
            Plate: MMPL0022  row: H  column: 09.
FEATURES             Location/Qualifiers
     source          1. .714
                     /organism="Macaca mulatta"
                     /mol_type="mRNA"
                     /db_xref="taxon:9544"
                     /sex="male"
                     /dev_stage="neonatal"
                     /clone_lib="MMPL"
                     /note="Organ: placenta"
ORIGIN

  Query Match             7.1%;  Score 607.8;  DB 6;  Length 714;
  Best Local Similarity   97.2%;  Pred. No. 7.9e-172;
  Matches  629;  Conservative    0;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
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Db        702 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 643

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
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Db        642 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 583

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
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Db        582 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 523

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
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Db        522 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 463

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
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Db        462 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 403

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
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Db        402 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 343

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
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Db        342 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 283

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT-CCATTCGCCATTCAGGCTGC 479
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Db        282 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTGCCATTCGCCATTCAGGCTGC 223

Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 163

Qy        540 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 599
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Db        162 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 103

Qy        600 GTAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
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Db        102 GTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 56


RESULT 12
BQ157858/c
LOCUS       BQ157858                 753 bp    mRNA    linear   EST 24-APR-2002
DEFINITION  NF103A09PL1F1067 Phosphate starved leaf Medicago truncatula cDNA
            clone NF103A09PL 5', mRNA sequence.
ACCESSION   BQ157858
VERSION     BQ157858.1  GI:20294915
KEYWORDS    EST.
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 753)
  AUTHORS   Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula phosphate-starved leaf library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Harrison MJ
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7325
            Fax: 580 221 7380
            Email: mjharrison@noble.org
            Insert Length: 753   Std Error: 0.00
            Plate: 103  row: A  column: 09
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:3880"
                     /clone="NF103A09PL"
                     /tissue_type="leaf"
                     /dev_stage="trifoliate"
                     /clone_lib="Phosphate starved leaf"
                     /note="Vector: Lambda Zap; At the trifoliate stage, M.
                     truncatula plants were transplanted to phosphate-free sand
                     and grown for a further 30 days.  During this 30 day
                     period, the plants were fertilized twice weekly with 1/2
                     Hoaglands solution containing only 20uM potassium
                     phosphate.  RNA was prepared from above ground tissues."
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ORIGIN

Query Match 7.1%; Score 607.8; DB 5; Length 753;
Best Local Similarity 97.2%; Pred. No. 8.1e-172;
Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

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Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
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Db        748 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 689

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
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Db        688 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 629

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 569

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 509

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 449

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
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Db        448 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 389

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
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Db        388 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 329

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT-CCATTCGCCATTCAGGCTGC 479
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Db        328 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTGCCATTCGCCATTCAGGCTGC 269

Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
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Db        268 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 209

Qy        540 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 599
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Qy        600 GTAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
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Db        148 GTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 102
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RESULT 13
BQ158943/c
LOCUS BQ158943 758 bp mRNA linear EST 24-APR-2002
DEFINITION NF095D07PL1F1060 Phosphate starved leaf Medicago truncatula cDNA clone NF095D07PL 5', mRNA sequence.
ACCESSION BQ158943
VERSION BQ158943.1 GI:20296000
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 758)
AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library
JOURNAL Unpublished (2000)
COMMENT Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 758 Std Error: 0.00
Plate: 095 row: D column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.

FEATURES Location/Qualifiers
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/db_xref="taxon:3880"
/clone="NF095D07PL"
/tissue_type="leaf"
/dev_stage="trifoliate"
/clone_lib="Phosphate starved leaf"
/note="Vector: Lambda Zap; At the trifoliate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."

ORIGIN

Query Match 7.1%; Score 607.8; DB 5; Length 758;
Best Local Similarity 97.2%; Pred. No. 8.1e-172;
Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

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Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 688

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
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Db        687 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 628

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 568

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 508

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 448

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
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Db        447 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 388

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
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Db        387 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 328

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT-CCATTCGCCATTCAGGCTGC 479
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Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
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Db        267 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 208

Qy        540 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 599
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Db        207 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 148

Qy        600 GTAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
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Db        147 GTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 101
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```
RESULT 14
BQ158750/c
LOCUS       BQ158750                764 bp    mRNA    linear   EST 24-APR-2002
DEFINITION  NF070F07PL1F1061 Phosphate starved leaf Medicago truncatula cDNA
            clone NF070F07PL 5', mRNA sequence.
ACCESSION   BQ158750
VERSION     BQ158750.1  GI:20295807
KEYWORDS    EST.
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 764)
  AUTHORS   Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula phosphate-starved leaf library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Harrison MJ
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7325
            Fax: 580 221 7380
            Email: mjharrison@noble.org
            Insert Length: 764   Std Error: 0.00
            Plate: 070  row: F  column: 07
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
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                     /dev_stage="trifoliate"
                     /clone_lib="Phosphate starved leaf"
                     /note="Vector: Lambda Zap; At the trifoliate stage, M.
                     truncatula plants were transplanted to phosphate-free sand
                     and grown for a further 30 days.  During this 30 day
                     period, the plants were fertilized twice weekly with 1/2
                     Hoaglands solution containing only 20uM potassium
                     phosphate.  RNA was prepared from above ground tissues."
ORIGIN

  Query Match             7.1%;  Score 607.8;  DB 5;  Length 764;
  Best Local Similarity   97.2%;  Pred. No. 8.1e-172;
  Matches  629;  Conservative    0;  Mismatches   17;  Indels    1;  Gaps    1;

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Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
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Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
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Db        628 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 569

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
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Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
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Db        508 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 449

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
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Db        448 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 389

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
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Db        388 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 329

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT-CCATTCGCCATTCAGGCTGC 479
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Db        328 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTGCCATTCGCCATTCAGGCTGC 269

Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
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Db        268 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 209

Qy        540 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 599
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Db        208 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 149

Qy        600 GTAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
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RESULT 15
BQ158875/c
LOCUS       BQ158875                771 bp    mRNA    linear   EST 24-APR-2002
DEFINITION  NF076G06PL1F1050 Phosphate starved leaf Medicago truncatula cDNA
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ACCESSION   BQ158875
VERSION     BQ158875.1  GI:20295932
KEYWORDS    EST.
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 771)
  AUTHORS   Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula phosphate-starved leaf library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Harrison MJ
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7325
            Fax: 580 221 7380
            Email: mjharrison@noble.org
            Insert Length: 771   Std Error: 0.00
            Plate: 076  row: G  column: 06
            Seq primer: TCACACAGGAAACAGCTATGAC.
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                     truncatula plants were transplanted to phosphate-free sand
                     and grown for a further 30 days.  During this 30 day
                     period, the plants were fertilized twice weekly with 1/2
                     Hoaglands solution containing only 20uM potassium
                     phosphate.  RNA was prepared from above ground tissues."
ORIGIN

  Query Match             7.1%;  Score 607.8;  DB 5;  Length 771;
  Best Local Similarity   97.2%;  Pred. No. 8.2e-172;
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Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

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Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 691

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 631

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 571

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 511

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 451

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 391

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 331

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT-CCATTCGCCATTCAGGCTGC 479
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Db        330 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTGCCATTCGCCATTCAGGCTGC 271

Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
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Db        270 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 211

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Db        210 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 151

Qy        600 GTAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
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Search completed: March 23, 2005, 17:05:35
Job time : 16279 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 08:17:54 ; Search time 2688 Seconds
(without alignments)
18805.309 Million cell updates/sec

Title: US-09-275-883-1_COPY_1_8539
Perfect score: 8539
Sequence: 1 ctgacgcgccctgtagcggc.....atactacaacaccaccacct 8539

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	8539	100.0	11282	4	AAD04741	Aad04741 Alphavira
3	8539	100.0	11282	5	AAF84024	Aaf84024 Complete
4	8539	100.0	11282	12	ADL71889	Adl71889 Temperatu
5	7657.2	89.7	13068	12	ADL71890	Adl71890 Temperatu
6	7657.2	89.7	15081	12	ADL71909	Adl71909 Expressio
7	7657.2	89.7	17753	12	ADL71910	Adl71910 Expressio
8	7637.4	89.4	9951	2	AAX77354	Aax77354 Polynucle
9	7637.4	89.4	9951	3	AAA90386	Aaa90386 Sindbis e
10	7637.4	89.4	9951	4	AAD04742	Aad04742 Alphavira
11	7637.4	89.4	9951	6	ABN86686	Abn86686 Nucleotid
12	7637.4	89.4	9951	6	ABV73174	Abv73174 Nucleotid
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14	7637.4	89.4	13905	2	AAX77358	Aax77358 Polynucle
15	7637.4	89.4	13905	3	AAA90390	Aaa90390 Plasmid p
16	7635.8	89.4	10524	2	AAX77355	Aax77355 Polynucle
17	7635.8	89.4	10524	3	AAA90387	Aaa90387 Plasmid p
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19	7634.8	89.4	8000	9	ADA50625	Ada50625 SINCG vir
20	7634.8	89.4	11703	13	ADR32077	Adr32077 Genomic D
21	7634.8	89.4	11703	13	ADR67767	Adr67767 Sindbis v
22	7634.8	89.4	11740	8	ABX81526	Abx81526 Sindbis v
23	7634.8	89.4	11740	9	ADA50626	Ada50626 Toto 1101
24	7634.2	89.4	16847	12	ADO07464	Ado07464 Japanese
25	7632.6	89.4	11927	2	AAX77356	Aax77356 Polynucle
26	7632.6	89.4	11927	3	AAA90388	Aaa90388 Plasmid p
27	7623.6	89.3	11703	3	AAC64506	Aac64506 Alphaviru
28	7620.4	89.2	11703	3	AAC64507	Aac64507 Alphaviru
29	7618.8	89.2	11703	2	AAV33476	Aav33476 Sindbis v
30	7617.2	89.2	8000	2	AAX59321	Aax59321 Sindbis v
31	7617.2	89.2	8000	2	AAX58571	Aax58571 Sindbis v
32	7617.2	89.2	8000	8	ABX81524	Abx81524 Sindbis v
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42	7610.8	89.1	16656	6	ABK46238	Abk46238 Eukaryoti
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ALIGNMENTS

RESULT 1
AAZ27850
ID AAZ27850 standard; cDNA; 11282 BP.
XX
AC AAZ27850;
XX
DT 23-DEC-1999 (first entry)
XX
DE Complete cDNA sequence of pCYTts.
XX
KW Gene expression system; cis-acting element; gene therapy;
KW temperature-sensitive RNA-dependent RNA polymerase;
KW inducible alphaviral gene expression system; pCYTts;
KW hormone-based gene control system; tetracycline gene control system; ss.
XX
OS Synthetic.
XX
PN WO9950432-A1.
XX
PD 07-OCT-1999.
XX
PF 25-MAR-1999; 99WO-IB000523.
XX
PR 27-MAR-1998; 98US-0079562P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (RENN/) RENNER W A.
PA (NIEB/) NIEBA L.
PA (BOOR/) BOORSMA M.
XX
PI Renner WA, Nieba L, Boorsma M;
XX
DR WPI; 1999-591327/50.
XX
PT A new system to regulate gene expression in eukaryotic cells.
XX
PS Claim 15; Fig 3; 99pp; English.
XX
CC This sequence represents the complete cDNA sequence for the vector
CC pCYTts. The invention relates to a DNA molecule comprising a
CC polynucleotide (I) encoding an RNA molecule. The encoded RNA comprises:
CC (a) at least one cis-acting element; (b) an open reading frame (ORF1)
CC encoding a non-cytopathic, temperature-sensitive RNA-dependent RNA

CC polymerase; and (c) a second sequence that is: (i) a protein-encoding ORF
CC (ORF2) that is in a translatable format after RNA-dependent RNA
CC replication event(s); (ii) a sequence complementary to the ORF2; or (iii)
CC a sequence encoding an untranslated RNA molecule. The pCYTts sequence is
CC an example of the DNA molecule, and is an inducible alphaviral gene
CC expression system. The invention is used in gene therapy and recombinant
CC technology to regulate expression of introduced genes. The invention does
CC not have the problems of toxicity and/or high basal level expression
CC associated with prior art tetracycline-based and hormone-based gene
CC control systems
XX
SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;

Query Match 100.0%; Score 8539; DB 2; Length 11282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
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Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120

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Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
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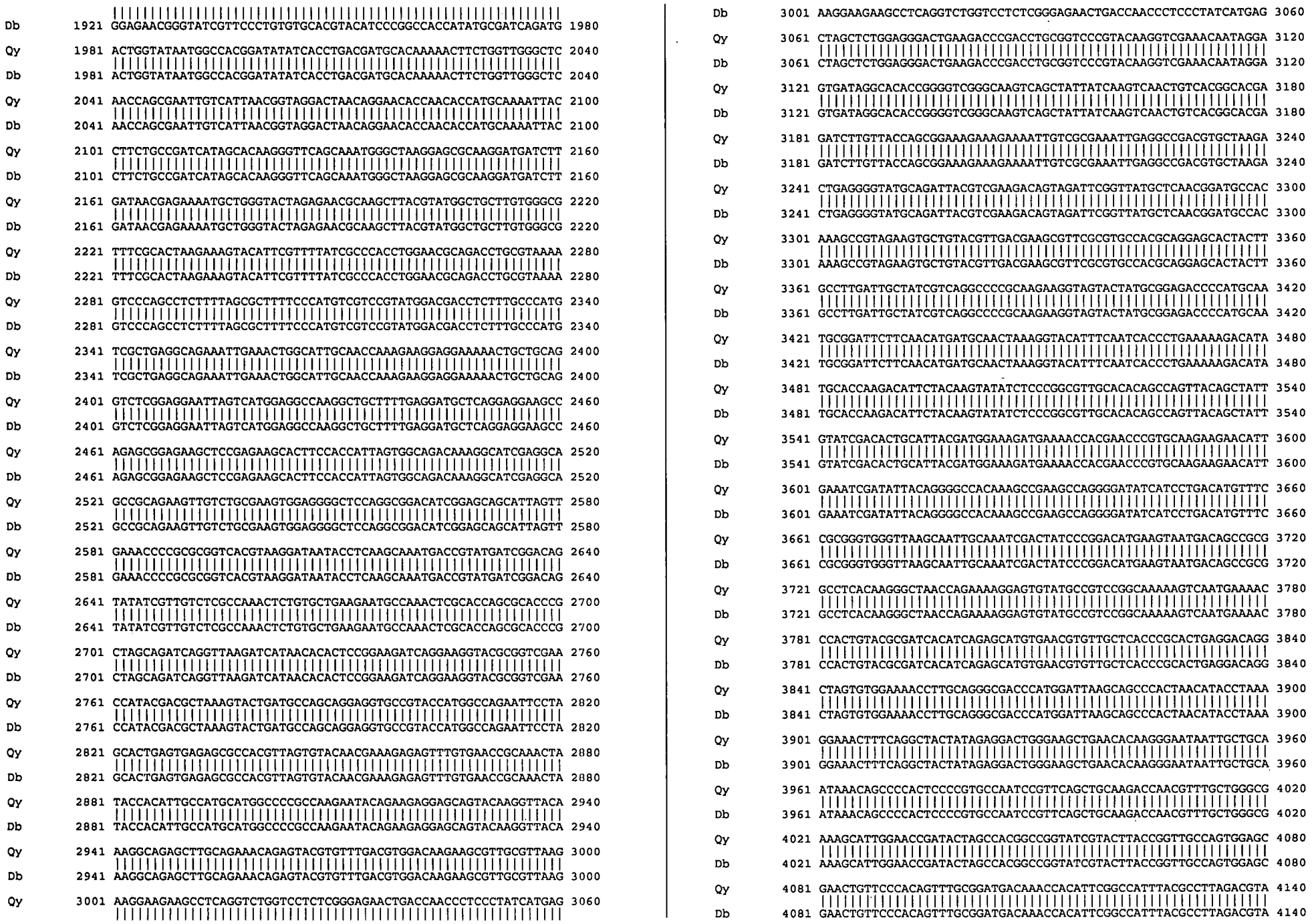
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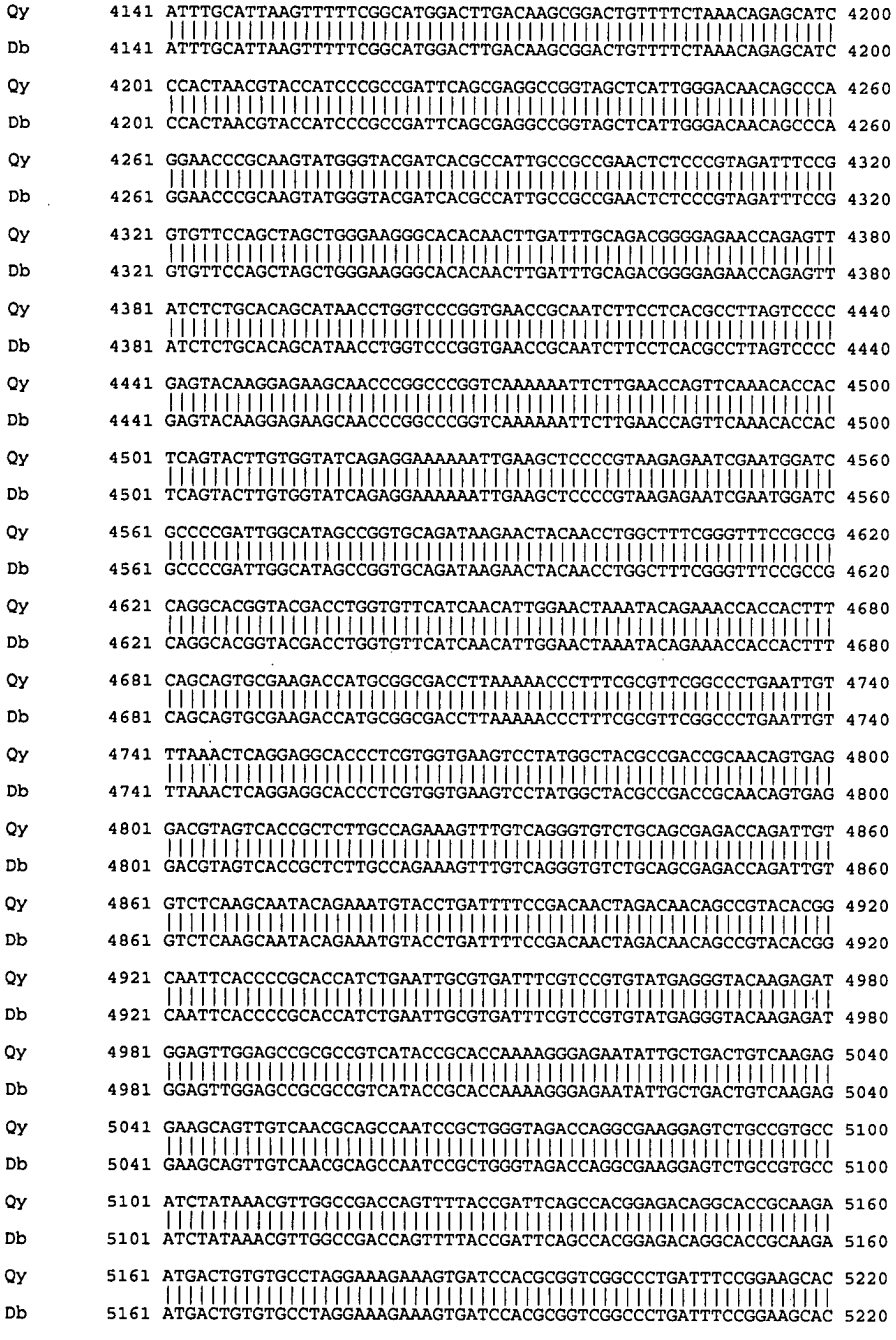
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Db      6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960
Qy      6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
Db      6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
Qy      7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
Db      7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
Qy      7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140
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Qy      7141 GCAACCTTCTGCCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200
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Qy      7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260
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Qy      7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320
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Qy      7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
Db      7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
Qy      7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440
Db      7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440
Qy      7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500
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Qy      7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560
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Db      7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620
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Db      7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680
Qy      7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
Db      7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
Qy      7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
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Qy      7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
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Qy      7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920
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Qy      7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980
Db      7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980
Qy      7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040
Db      7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040
Qy      8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
Db      8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
Qy      8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160
Db      8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160
Qy      8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220
Db      8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220
Qy      8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280
Db      8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280
Qy      8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340
Db      8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340
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Qy      8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460
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Db      8461 GAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCATCTGACTAA 8520
```

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Qy       8521 TACTACAACACCACCACCT 8539
             ||||||||||||||||||||
Db       8521 TACTACAACACCACCACCT 8539
```

RESULT 2
AAD04741
ID AAD04741 standard; cDNA; 11282 BP.
XX
AC AAD04741;
XX
DT 17-JUL-2001 (first entry)
XX
DE Alphaviral vector pCYTts cDNA.
XX
KW pCYTts; alphaviral vector; vaccine; therapy; cancer; antiparasitic;
KW antimalarial; anticancer; anti-HIV; antiviral; infectious disease;
KW Human immunodeficiency virus; HIV; influenza; passive immunisation;
KW carcinoma; liver; skin; stomach; ovarian tumour; ss.
XX
OS Rous sarcoma virus.
OS Alphavirus.
OS Unidentified.
OS Chimeric.
XX
PN WO200130989-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-IB001557.
XX
PR 27-OCT-1999; 99US-0161796P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (RENN/) RENNER W A.
PA (NIEB/) NIEBA L.
XX
PI Renner WA, Nieba L;
XX
DR WPI; 2001-308631/32.
XX
PT Preparing alphaviral vectors with mutations in a selected gene, for use
PT as vaccines, particularly against pathogens that mutate rapidly,
PT comprises replicating in the presence of a nucleoside analog.
XX
PS Claim 6; Fig 3; 103pp; English.
XX
CC The present invention relates to a method for preparing viral vectors
CC which comprises inserting a gene of interest into an alphaviral vector
CC such as pCYTts, pSinRep5 and replicating the vector in the presence of
CC alphaviral replicase and nucleoside analogues (5'azacytidine (AZT), FU-
CC 5' fluorouridine) to produce a modified gene of interest. The replication
CC is repeated until the modified gene in 90 % of the vector population
CC contain a mutation in the modified gene which is 90-99 % identical with
CC the gene of interest. The vector populations are used in vaccines for
CC treatment or prevention of a wide variety of infectious diseases (viral
CC or parasitic, e.g. human immuno deficiency virus (HIV), influenza,
CC Trypanosoma or Plasmodium) and cancers such as liver carcinoma, stomach
CC carcinoma, skin carcinoma and ovarian tumours. Vaccines containing the
CC mutant populations will therefore be effective against viral escape
CC mutants. Mutagenesis in a eukaryotic cell ensures that expressed proteins
CC are correctly glycosylated. Antisera raised against the vaccines can be
CC used for passive immunisation. The present cDNA sequence is an alphaviral
CC vector pCYTts. The vector contains Rous Sarcoma Virus promoter, cis-
CC acting sequence elements, non-structural proteins 1-4, gene of interest,
CC alphavirus subgenomic promoter, ampicillin resistance marker for
CC selection and a CoIE1 sequence for bacterial amplification
XX
SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;

Query Match 100.0%; Score 8539; DB 4; Length 11282;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
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Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCG 480

Qy        481 CAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        541 GGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTG 600

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAACAAAAGCTGGCTAG 660

Qy        661 TGGATCCAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        721 CATGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTAC 780
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Qy        781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        841 TTCCGCATTGCAGAGATATTGTATTTAAGTGCCCTACCTCGATACCGTCGAGATTGACGG 900

Qy        901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960
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Db        901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960

Qy        961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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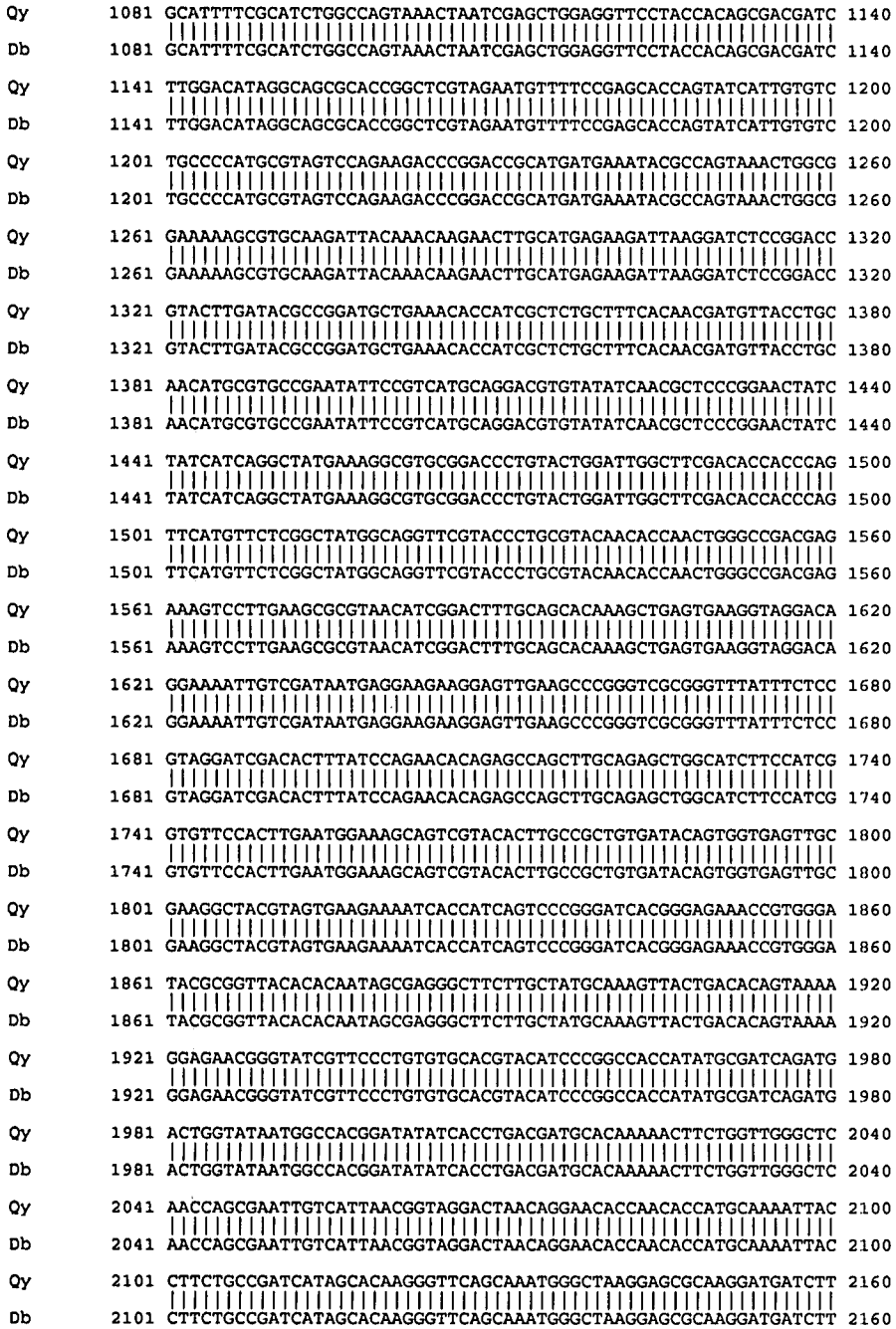
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Qy 1141 TTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATTGTGTC 1200
Db 1141 TTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATTGTGTC 1200
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Db 1321 GTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATGTTACCTGC 1380
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Qy 2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520
Db 2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520
Qy 2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580
Db 2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580
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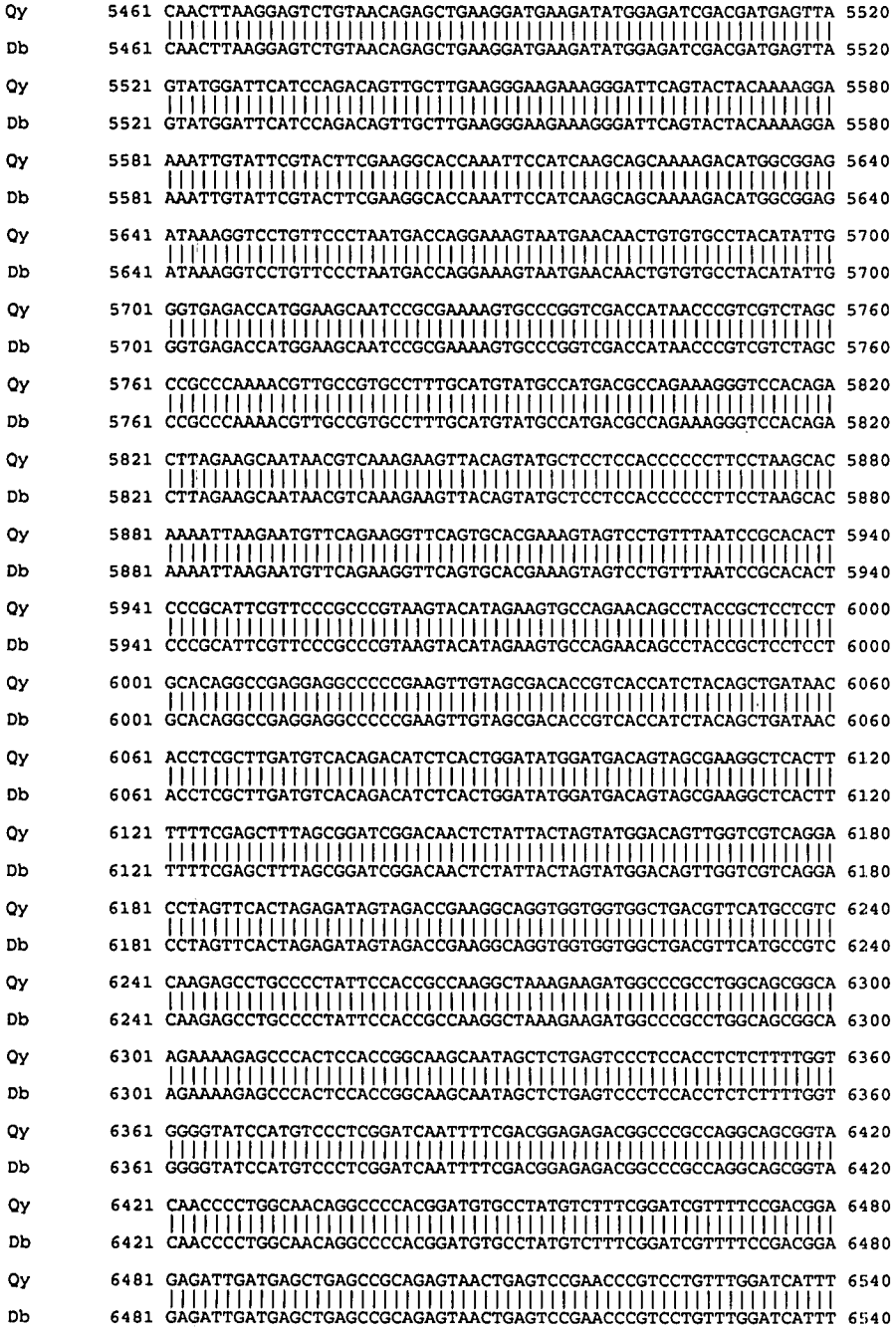
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RESULT 3
AAF84024
ID   AAF84024 standard; cDNA; 11282 BP.
XX
AC   AAF84024;
XX
DT   22-AUG-2001  (first entry)
XX
DE   Complete cDNA sequence of plasmid pCYTt.
XX
KW   pCYTt; cellular; taxol; gene therapy; RNA replication; endogenous gene;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO200142442-A2.
XX
PD   14-JUN-2001.
XX
PF   08-DEC-2000; 2000WO-IB001841.
XX
PR   10-DEC-1999;   99US-0169988P.
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI   Hennecke F,  Renner WA;
XX
DR   WPI; 2001-381672/40.
XX
PT   Modifying endogenous target gene expression in eukaryotic cell for
PT   performing gene therapy, involves inserting exogenous polynucleotides in
PT   gene to produce recombinant eukaryotic host cell and culturing the cell.
XX
PS   Disclosure; Fig 8A-D; 131pp; English.
XX
CC   The invention relates to a method of modifying expression characteristics
CC   of an endogenous target gene within a genome of a eukaryotic cell or
CC   producing a polypeptide encoded by the target gene of a eukaryotic cell.
CC   The method involves inserting exogenous polynucleotides in 5' and 3'
CC   regions flanking the coding region of target gene to produce a
CC   recombinant eukaryotic host cell, and culturing the cell. The method is
CC   useful for producing cells which exhibit increased expression of
CC   endogenous genes which lead to the production of additional products, and
CC   for amplifying endogenous genes involved in the production of cellular
CC   products such as taxol. The method is also useful for producing
CC   biological products, and their derivatives, and for regulating the
CC   activity of target genes by modifying the expression of regulatory
CC   proteins involved in the regulation of the target genes. The method or a
CC   DNA vector system is useful for performing gene therapy on an individual
CC   (e.g., domesticated animal or human). The present sequence represents the
CC   complete cDNA sequence of a vector pCYTts, a DNA vector system for
CC   modifying the expression characteristics of an endogenous target gene
CC   within the genome of a eukaryotic cell comprising a 5' targeting
CC   construct and a 3' targeting construct, where the 5' and 3' targeting
CC   construct encode genetic elements required for RNA replication
XX
SQ   Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 8539;  DB 5;  Length 11282;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 8539;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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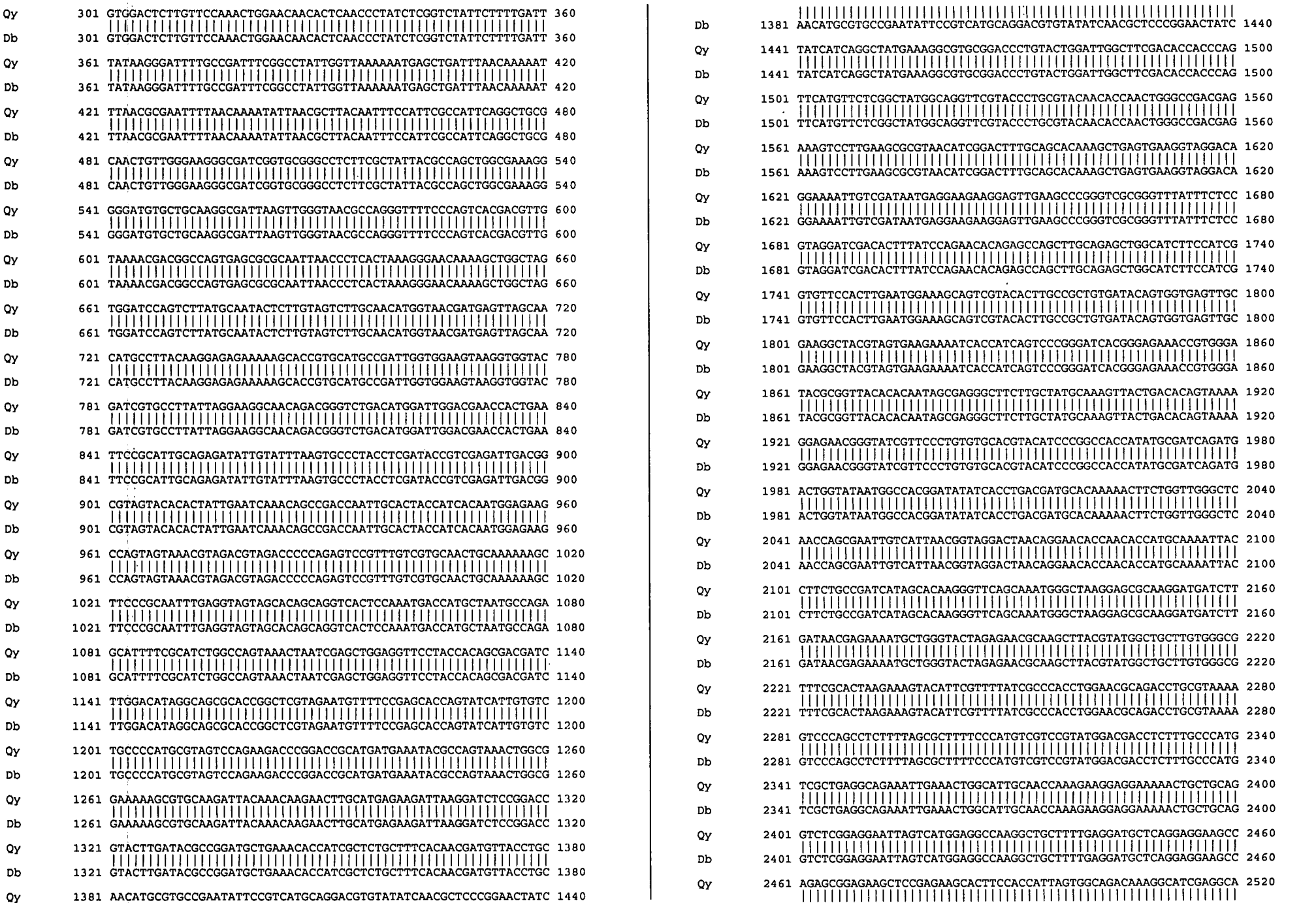
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Qy 781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAA 840
Db 781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAA 840
Qy 841 TTCCGCATTGCAGAGATATTGTATTTAAGTGCCCTACCTCGATACCGTCGAGATTGACGG 900
Db 841 TTCCGCATTGCAGAGATATTGTATTTAAGTGCCCTACCTCGATACCGTCGAGATTGACGG 900
Qy 901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960
Db 901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960
Qy 961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020
Db 961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020
Qy 1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080
Db 1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080
Qy 1081 GCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGACGATC 1140
Db 1081 GCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGACGATC 1140
Qy 1141 TTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATTGTGTC 1200
Db 1141 TTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATTGTGTC 1200
Qy 1201 TGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTAAACTGGCG 1260
Db 1201 TGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTAAACTGGCG 1260
Qy 1261 GAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATCTCCGGACC 1320
Db 1261 GAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATCTCCGGACC 1320
Qy 1321 GTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATGTTACCTGC 1380
Db 1321 GTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATGTTACCTGC 1380
Qy 1381 AACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCGGAACTATC 1440
Db 1381 AACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCGGAACTATC 1440
Qy 1441 TATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACACCACCCAG 1500
Db 1441 TATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACACCACCCAG 1500
Qy 1501 TTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGGCCGACGAG 1560
Db 1501 TTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGGCCGACGAG 1560
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Db 1681 GTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATCTTCCATCG 1740
Qy 1741 GTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGGTGAGTTGC 1800
Db 1741 GTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGGTGAGTTGC 1800
Qy 1801 GAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAACCGTGGGA 1860
Db 1801 GAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAACCGTGGGA 1860
Qy 1861 TACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACACAGTAAAA 1920
Db 1861 TACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACACAGTAAAA 1920
Qy 1921 GGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCGATCAGATG 1980
Db 1921 GGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCGATCAGATG 1980
Qy 1981 ACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGGTTGGGCTC 2040
Db 1981 ACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGGTTGGGCTC 2040
Qy 2041 AACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGCAAAATTAC 2100
Db 2041 AACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGCAAAATTAC 2100
Qy 2101 CTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGGATGATCTT 2160
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Db 2161 GATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCTTGTGGGCG 2220
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Qy 2341 TCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAACTGCTGCAG 2400
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Qy 2401 GTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGGAGGAAGCC 2460
Db 2401 GTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGGAGGAAGCC 2460
Qy 2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520

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Db      2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520
Qy      2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580
Db      2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580
Qy      2581 GAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGATCGGACAG 2640
Db      2581 GAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGATCGGACAG 2640
Qy      2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAGCGCACCCG 2700
Db      2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAGCGCACCCG 2700
Qy      2701 CTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACGCGGTCGAA 2760
Db      2701 CTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACGCGGTCGAA 2760
Qy      2761 CCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAGAATTCCTA 2820
Db      2761 CCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAGAATTCCTA 2820
Qy      2821 GCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACCGCAAACTA 2880
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Qy      2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940
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Qy      2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000
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Qy      3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060
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Db      3061 CTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAACAATAGGA 3120
Qy      3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180
Db      3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180
Qy      3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
Db      3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
Qy      3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300
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Qy      3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360
Db      3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360
Qy      3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
Db      3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
Qy      3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
Db      3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
Qy      3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
Db      3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
Qy      3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
Db      3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
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Db      3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660
Qy      3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720
Db      3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720
Qy      3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780
Db      3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780
Qy      3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840
Db      3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840
Qy      3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900
Db      3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900
Qy      3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960
Db      3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960
Qy      3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
Db      3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
Qy      4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
Db      4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
Qy      4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140
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Qy      4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260
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Qy      4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320
Db      4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320
Qy      4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380
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Qy      4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440
Db      4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440
Qy      4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500
Db      4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500
Qy      4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560
Db      4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560
Qy      4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620
Db      4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620
Qy      4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680
Db      4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680
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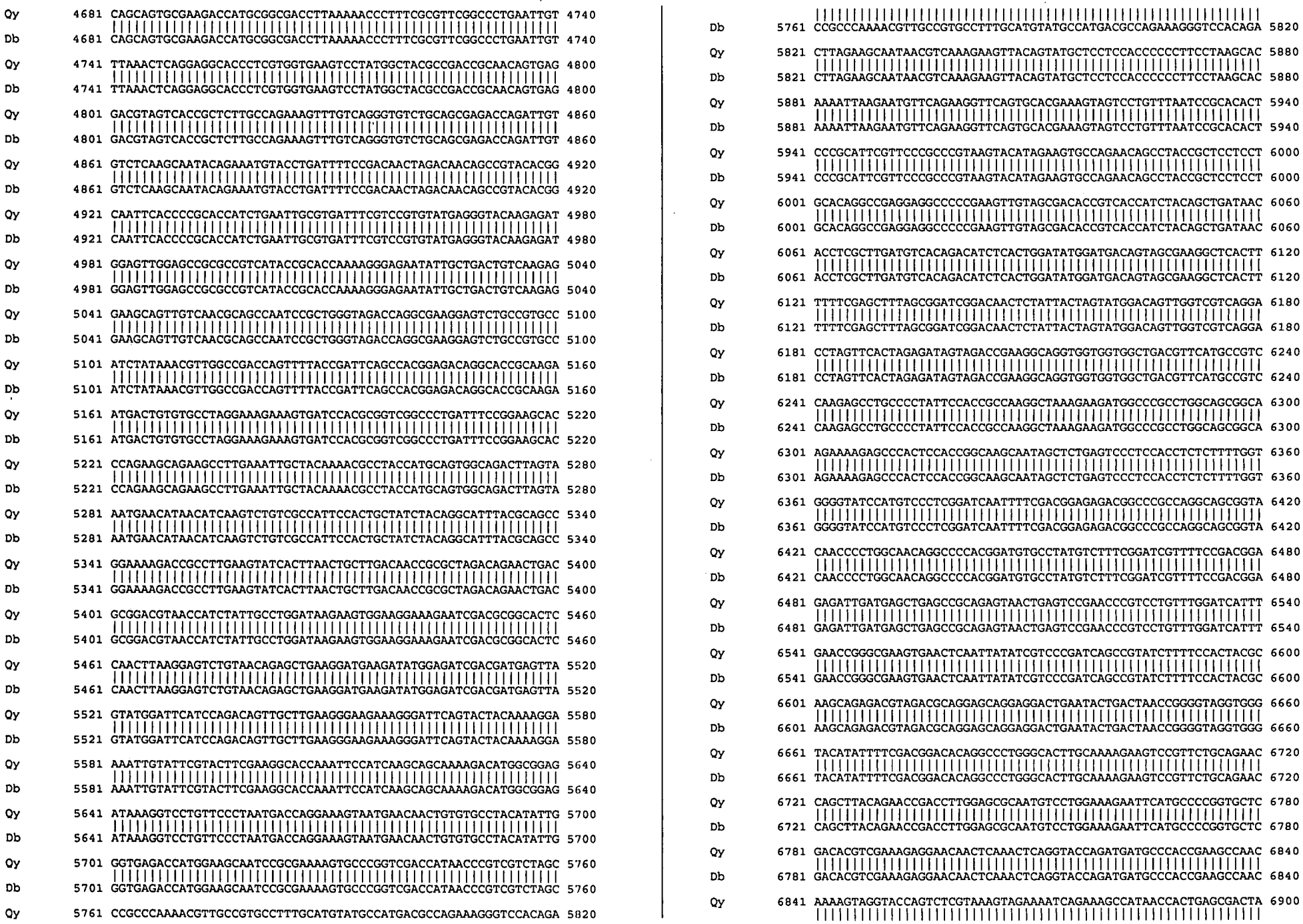

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Qy       6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960
Qy       6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
Qy       7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
Qy       7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140
Qy       7141 GCAACCTTCTGCCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7141 GCAACCTTCTGCCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200
Qy       7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260
Qy       7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320
Qy       7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
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Db       7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
Qy       7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440
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Db       7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440
Qy       7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500
Qy       7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560
Qy       7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620
Qy       7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680
Qy       7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
Qy       7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
Qy       7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
Qy       7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
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Db       8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
Qy       8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160
Qy       8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220
Qy       8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280
Qy       8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340
Qy       8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400
Qy       8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460
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Db       8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460
Qy       8461 GAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCATCTGACTAA 8520
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Db       8461 GAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCATCTGACTAA 8520
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Db       8521 TACTACAACACCACCACCT 8539
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RESULT 4
ADL71889
ID   ADL71889 standard; cDNA; 11282 BP.
XX
AC   ADL71889;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Temperature inducible alphavirus vector pCytTs.
XX
KW   Gene expression; vector; pCytTS; ss.
XX
OS   Rous sarcoma virus.
OS   Alphavirus.
OS   Chimeric.
XX
PN   WO2004018506-A2.
XX
PD   04-MAR-2004.
XX
PF   21-AUG-2003; 2003WO-EP009291.
XX
PR   22-AUG-2002; 2002US-0404928P.
PR   11-DEC-2002; 2002US-0432259P.
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI   Ivanova L,  Renner WA,  Saudan P;
XX
DR   WPI; 2004-226795/21.
XX
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PT New nucleic acid molecule comprising first, second and third
PT polynucleotide elements, useful for regulating the expression of a
PT polypeptide or an untranslated RNA molecule.
XX
PS Example 1; SEQ ID NO 1; 112pp; English.
XX
CC The present sequence is that of the tightly regulated temperature
CC inducible alphavirus expression system pCytTS containing a Rous sarcoma
CC virus (RSV) promoter. The vector can be used to drive transcription of
CC mRNA from a nucleic acid molecule of the invention. A claimed nucleic
CC acid molecule comprises: (A) a first polynucleotide element which encodes
CC an RNA molecule comprising (a) at least one cis-acting sequence element,
CC (b) a first nucleotide sequence comprising a first open reading frame,
CC the first open reading frame having a nucleotide sequence encoding an RNA
CC -dependent RNA polymerase, and (c) at least one second nucleotide
CC sequence comprising (i) a second open reading frame (S1) encoding a
CC polypeptide, (ii) a nucleotide sequence complementary to all or a part of
CC the second open reading frame (S1) and (iii) a nucleotide sequence
CC encoding an untranslated RNA molecule or its complement, where the second
CC nucleotide sequence is operably linked to a promoter which is recognised
CC by the RNA-dependent RNA polymerase; (B) a second polynucleotide element
CC comprising an origin of replication; and (C) a third polynucleotide
CC element encoding a replication initiation factor capable of recognising
CC the origin of replication. The nucleic acid molecule, expression systems
CC and vector systems of the invention allow the production of polypeptides
CC and untranslated RNA molecules in host cells. In a specific embodiment,
CC the invention includes the combination of a herpesvirus mini-replicon
CC unit, i.e. the cis-acting replication origin oriP and the cis- or trans-
CC acting gene product EBNA-1 with pCysTS ADL71909-ADL71910. Due to the
CC presence of OriP and EBNA-1, the novel vector is maintained episomally in
CC the form of several DNA copies in cell nuclei. These multiple DNA copies
CC may be transcribed from the RSV promoter into CysTS RNA replicons, but
CC remain inactive unless cells are shifted to a certain temperature. Only
CC after temperature induction does replicon replication occur, followed by
CC RNA accumulation and translation in the cell cytoplasm, and production of
CC the polypeptide of interest.
XX
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Query Match 100.0%; Score 8539; DB 12; Length 11282;
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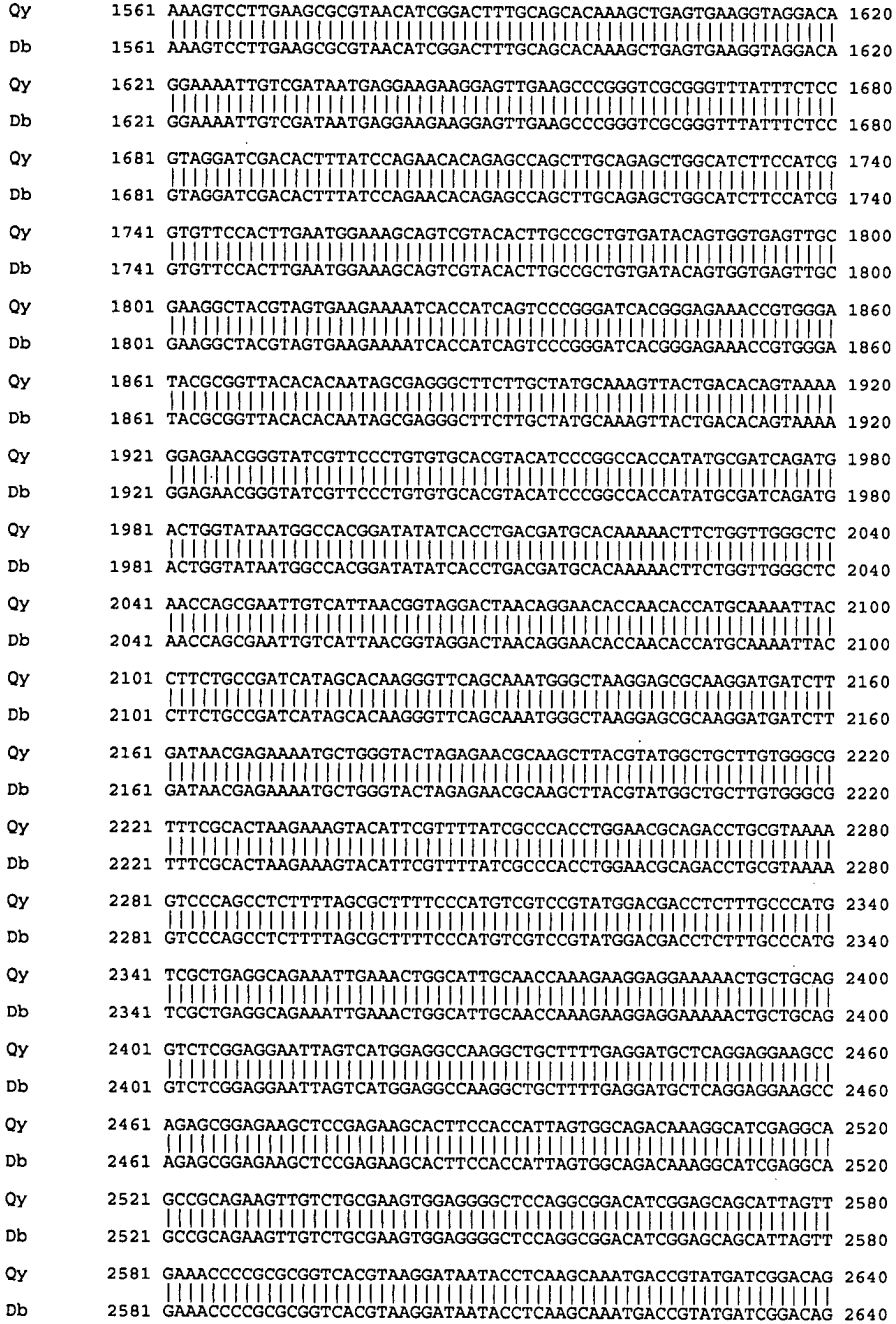
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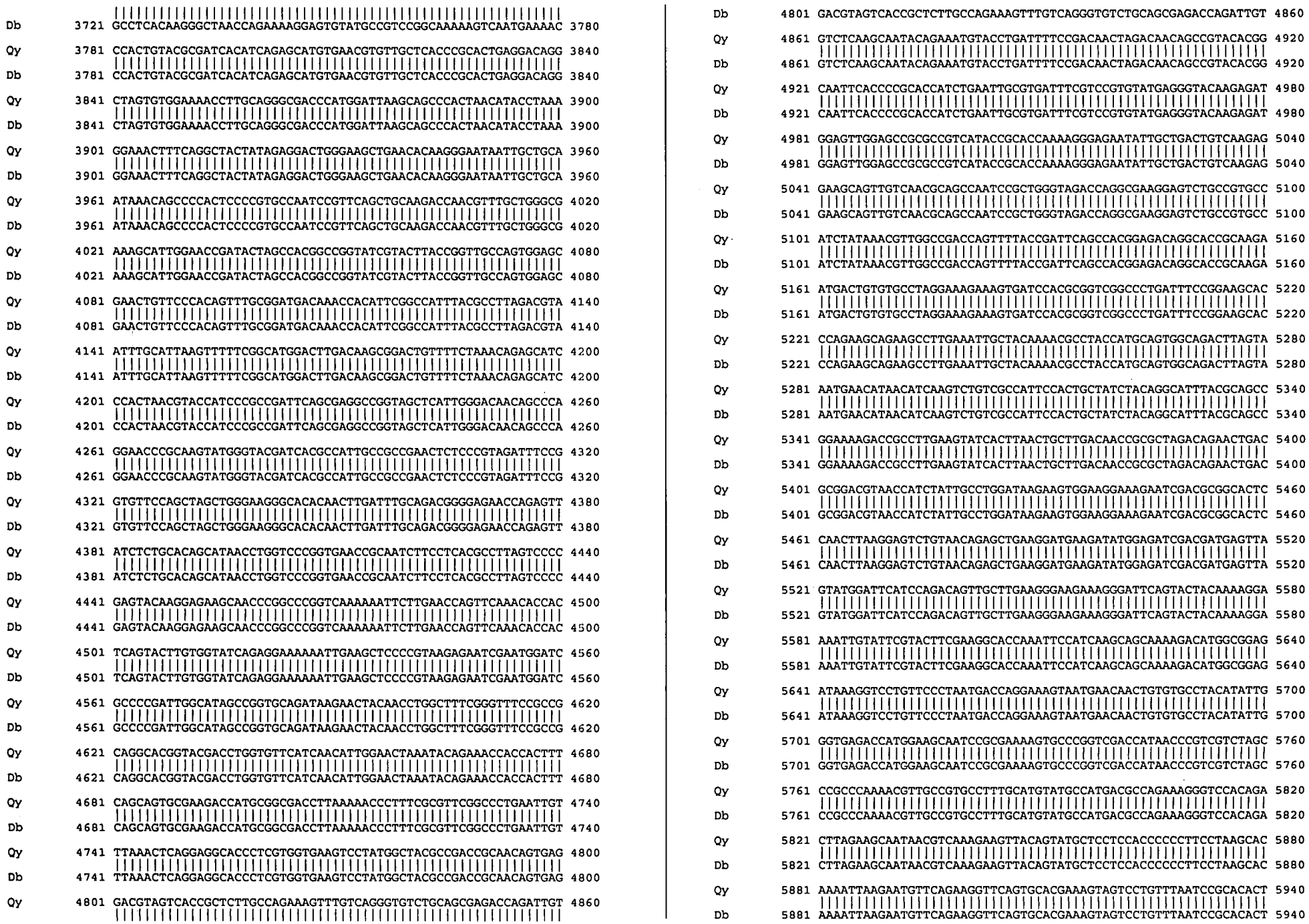

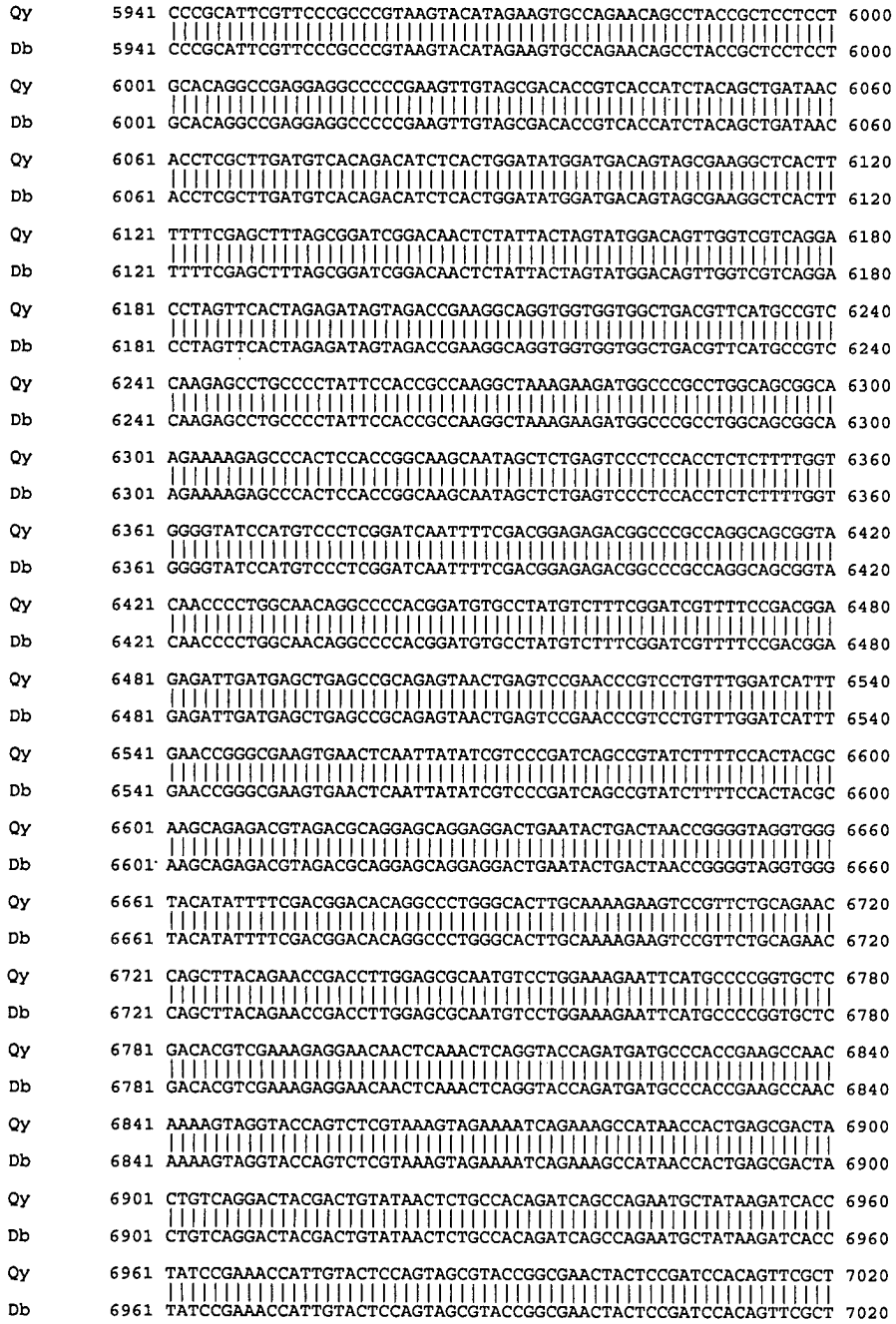
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Db 7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680
Qy 7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
Db 7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
Qy 7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
Db 7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
Qy 7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
Db 7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
Qy 7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920
Db 7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920
Qy 7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980
Db 7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980
Qy 7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040
Db 7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040
Qy 8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
Db 8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
Qy 8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160

Qy       8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220

Qy       8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280

Qy       8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340

Qy       8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400

Qy       8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460

Qy       8461 GAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCATCTGACTAA 8520
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8461 GAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCATCTGACTAA 8520

Qy       8521 TACTACAACACCACCACCT 8539
                ||||||||||||||||||
Db       8521 TACTACAACACCACCACCT 8539
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RESULT 5
ADL71890
ID ADL71890 standard; cDNA; 13068 BP.
XX
AC ADL71890;
XX
DT 20-MAY-2004 (first entry)
XX
DE Temperature inducible alphavirus vector pCytTs2.1.
XX
KW Gene expression; vector; pCytTS2.1; ss.
XX
OS Cytomegalovirus.
OS Alphavirus.
OS Chimeric.
XX
PN WO2004018506-A2.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-EP009291.
XX
PR 22-AUG-2002; 2002US-0404928P.
PR 11-DEC-2002; 2002US-0432259P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Ivanova L, Renner WA, Saudan P;
XX
DR WPI; 2004-226795/21.
XX
PT New nucleic acid molecule comprising first, second and third
PT polynucleotide elements, useful for regulating the expression of a
PT polypeptide or an untranslated RNA molecule.
XX
PS Example 1; SEQ ID NO 2; 112pp; English.
XX
CC The present sequence is that of the tightly regulated temperature
CC inducible alphavirus expression system pCytTS2.1 containing a
CC cytomegalovirus (CMV). The vector can be used to drive transcription of
CC mRNA from a nucleic acid molecule of the invention. A claimed nucleic
CC acid molecule comprises: (A) a first polynucleotide element which encodes
CC an RNA molecule comprising (a) at least one cis-acting sequence element,
CC (b) a first nucleotide sequence comprising a first open reading frame,
CC the first open reading frame having a nucleotide sequence encoding an RNA
CC -dependent RNA polymerase, and (c) at least one second nucleotide
CC sequence comprising (i) a second open reading frame (S1) encoding a
CC polypeptide, (ii) a nucleotide sequence complementary to all or a part of
CC the second open reading frame (S1) and (iii) a nucleotide sequence
CC encoding an untranslated RNA molecule or its complement, where the second
CC nucleotide sequence is operably linked to a promoter which is recognised
CC by the RNA-dependent RNA polymerase; (B) a second polynucleotide element
CC comprising an origin of replication; and (C) a third polynucleotide
CC element encoding a replication initiation factor capable of recognising
CC the origin of replication. The nucleic acid molecule, expression systems
CC and vector systems of the invention allow the production of polypeptides
CC and untranslated RNA molecules in host cells. In a specific embodiment,
CC the invention includes the combination of a herpesvirus mini-replicon
CC unit, i.e. the cis-acting replication origin oriP and the cis- or trans-
CC acting gene product EBNA-1 with pCysTS. Due to the presence of OriP and
CC EBNA-1, the novel vector is maintained episomally in the form of several
CC DNA copies in cell nuclei. These multiple DNA copies may be transcribed
CC from the CMV promoter into CysTS2.1 RNA replicons, but remain inactive
CC unless cells are shifted to a certain temperature. Only after temperature
CC induction does replicon replication occur, followed by RNA accumulation
CC and translation in the cell cytoplasm, and production of the polypeptide
CC of interest.
XX
SQ Sequence 13068 BP; 3555 A; 3379 C; 3204 G; 2930 T; 0 U; 0 Other;

Query Match 89.7%; Score 7657.2; DB 12; Length 13068;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7642; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 928

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        929 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 988

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        989 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1048

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1049 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1108

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1109 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1168

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       1169 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATATGCCAGTA 1228

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1229 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1288

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1289 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1348

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1349 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1408

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1409 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1468
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Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1469 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1528

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1529 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1588

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1589 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1648

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1649 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1708

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1709 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1768

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1769 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1828

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1829 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1888

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1889 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1948

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1949 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2008

Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2009 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2068

Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2069 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2128

Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2129 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2188

Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2189 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2248

Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2249 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2308

Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2309 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2368

Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2369 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2428

Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2429 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2488

Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2489 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2548

Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2549 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2608

Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2609 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2668

Qy       2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2669 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2728

Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2729 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2788

Qy       2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2789 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2848

Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2849 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2908

Qy       2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2909 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2968

Qy       2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2969 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3028

Qy       3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3029 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3088

Qy       3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3089 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3148

Qy       3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3149 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3208

Qy       3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3209 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3268

Qy       3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3269 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3328

Qy       3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3329 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3388

Qy       3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3389 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3448

Qy       3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3449 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3508

Qy       3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3509 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3568

Qy       3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3569 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3628

Qy       3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       3629 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3688
Qy       3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
Db       3689 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3748
Qy       3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
Db       3749 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3808
Qy       3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
Db       3809 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCTCACTAACA 3868
Qy       3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
Db       3869 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3928
Qy       3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
Db       3929 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3988
Qy       4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
Db       3989 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4048
Qy       4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
Db       4049 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4108
Qy       4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
Db       4109 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4168
Qy       4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
Db       4169 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4228
Qy       4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
Db       4229 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4288
Qy       4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
Db       4289 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4348
Qy       4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
Db       4349 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4408
Qy       4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
Db       4409 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCGAAAAATTCTTGAACCAGTTCA 4468
Qy       4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
Db       4469 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4528
Qy       4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
Db       4529 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4588
Qy       4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
Db       4589 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4648
Qy       4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
Db       4649 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4708
Qy       4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
Db       4709 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4768

Qy       4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
Db       4769 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4828
Qy       4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
Db       4829 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4888
Qy       4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
Db       4889 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4948
Qy       4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
Db       4949 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5008
Qy       5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
Db       5009 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5068
Qy       5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
Db       5069 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5128
Qy       5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
Db       5129 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5188
Qy       5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
Db       5189 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5248
Qy       5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
Db       5249 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5308
Qy       5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
Db       5309 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5368
Qy       5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
Db       5369 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5428
Qy       5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
Db       5429 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5488
Qy       5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
Db       5489 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5548
Qy       5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
Db       5549 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5608
Qy       5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
Db       5609 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5668
Qy       5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
Db       5669 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5728
Qy       5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
Db       5729 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5788
Qy       5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
Db       5789 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5848
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Qy       5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5849 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5908

Qy       5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5909 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5968

Qy       5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5969 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6028

Qy       6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6029 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6088

Qy       6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6089 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6148

Qy       6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6149 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6208

Qy       6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6209 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6268

Qy       6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6269 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6328

Qy       6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6329 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6388

Qy       6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6389 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6448

Qy       6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6449 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6508

Qy       6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6509 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6568

Qy       6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6569 CTCTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6628

Qy       6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6629 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6688

Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6689 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6748

Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6749 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6808

Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6809 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6868

Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6869 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6928

Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6929 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6988

Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6989 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7048

Qy       7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7049 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7108

Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7109 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7168

Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7169 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7228

Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7229 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7288

Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7289 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7348

Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7349 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7408

Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7409 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7468

Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7469 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7528

Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7529 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7588

Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7589 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7648

Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7649 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7708

Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7709 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7768

Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7769 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7828

Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7829 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7888

Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7889 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7948

Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7949 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8008

Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       8009 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8068

Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8069 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8128

Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8129 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8188

Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8189 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8248

Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8249 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8308

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8309 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8368

Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8369 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8428

Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8429 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8488

Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
             |||||||||||| ||||||||||||||
Db       8489 CTGACTAATACCACAACACCACCACCT 8515


RESULT 6
ADL71909
ID   ADL71909 standard; cDNA; 15081 BP.
XX
AC   ADL71909;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Expression vector pCytTs-OriP.
XX
KW   Gene expression; vector; pCytTS; ss.
XX
OS   Alphavirus.
OS   Human herpesvirus 4.
OS   Chimeric.
XX
PN   WO2004018506-A2.
XX
PD   04-MAR-2004.
XX
PF   21-AUG-2003; 2003WO-EP009291.
XX
PR   22-AUG-2002; 2002US-0404928P.
PR   11-DEC-2002; 2002US-0432259P.
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI   Ivanova L,  Renner WA,  Saudan P;
XX
DR   WPI; 2004-226795/21.
XX
PT   New nucleic acid molecule comprising first, second and third
PT   polynucleotide elements, useful for regulating the expression of a
PT   polypeptide or an untranslated RNA molecule.
XX
PS   Example 2; SEQ ID NO 21; 112pp; English.
XX
CC   The present sequence is that of expression vector pCytTs-OriP. A claimed
CC   nucleic acid molecule comprises: (A) a first polynucleotide element which
CC   encodes an RNA molecule comprising (a) at least one cis-acting sequence
CC   element, (b) a first nucleotide sequence comprising a first open reading
CC   frame, the first open reading frame having a nucleotide sequence encoding
CC   an RNA-dependent RNA polymerase, and (c) at least one second nucleotide
CC   sequence comprising (i) a second open reading frame (S1) encoding a
CC   polypeptide, (ii) a nucleotide sequence complementary to all or a part of
CC   the second open reading frame (S1) and (iii) a nucleotide sequence
CC   encoding an untranslated RNA molecule or its complement, where the second
CC   nucleotide sequence is operably linked to a promoter which is recognised
CC   by the RNA-dependent RNA polymerase; (B) a second polynucleotide element
CC   comprising an origin of replication; and (C) a third polynucleotide
CC   element encoding a replication initiation factor capable of recognising
CC   the origin of replication. The nucleic acid molecule, expression systems
CC   and vector systems of the invention allow the production of polypeptides
CC   and untranslated RNA molecules in host cells. In a specific embodiment,
CC   the invention includes the combination of a herpesvirus mini-replicon
CC   unit, e.g. the cis-acting replication origin oriP from Epstein Barr
CC   virus, with pCysTS ADL71889, creating pCytTs-OriP. Due to the presence of
CC   OriP, the novel vector is maintained episomally in the form of several
CC   DNA copies in cell nuclei. These multiple DNA copies may be transcribed
CC   from a Rous sarcoma virus or cytomegalovirus promoter into pCysTS RNA
CC   replicons, but remain inactive unless cells are shifted to a certain
CC   temperature. Only after temperature induction does replicon replication
CC   occur, followed by RNA accumulation and translation in the cell
CC   cytoplasm, and production of the polypeptide of interest.
XX
SQ   Sequence 15081 BP; 4101 A; 3826 C; 3676 G; 3478 T; 0 U; 0 Other;

  Query Match             89.7%;  Score 7657.2;  DB 12;  Length 15081;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7642;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 928

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        929 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 988

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        989 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1048

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1049 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1108

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1109 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1168

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       1169 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATATGCCAGTA 1228

Qy       1253 AACTGGCGGAAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1229 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1288

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1289 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1348

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1349 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1408

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1409 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1468
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Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1469 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1528

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1529 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1588

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1589 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1648

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1649 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1708

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1709 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1768

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1769 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1828

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1829 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1888

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1889 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1948

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1949 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2008

Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2009 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2068

Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2069 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2128

Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2129 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2188

Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2189 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2248

Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2249 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2308

Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2309 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2368

Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2369 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2428

Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2429 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2488

Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2489 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2548

Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2549 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2608

Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2609 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2668

Qy       2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2669 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2728

Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2729 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2788

Qy       2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2789 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2848

Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2849 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2908

Qy       2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2909 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2968

Qy       2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2969 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3028

Qy       3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3029 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3088

Qy       3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3089 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3148

Qy       3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3149 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3208

Qy       3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3209 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3268

Qy       3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3269 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3328

Qy       3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3329 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3388

Qy       3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3389 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3448

Qy       3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3449 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3508

Qy       3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3509 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3568

Qy       3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3569 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3628

Qy       3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3629 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3688
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Db       3629 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3688

Qy       3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3689 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3748

Qy       3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3749 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3808

Qy       3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
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Qy       3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3869 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3928

Qy       3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3929 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3988

Qy       4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3989 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4048

Qy       4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4049 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4108

Qy       4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4109 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4168

Qy       4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4169 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4228

Qy       4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4229 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4288

Qy       4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4289 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4348

Qy       4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4349 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4408

Qy       4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
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Db       4409 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCGAAAAATTCTTGAACCAGTTCA 4468

Qy       4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
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Qy       4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4529 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4588

Qy       4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
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Qy       4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
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Qy       4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
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Qy       4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
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Db       4769 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4828

Qy       4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4829 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4888

Qy       4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
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Qy       4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
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Db       4949 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5008

Qy       5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5009 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5068

Qy       5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5069 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5128

Qy       5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5129 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5188

Qy       5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5189 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5248

Qy       5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5249 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5308

Qy       5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5309 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5368

Qy       5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5369 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5428

Qy       5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5429 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5488

Qy       5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5489 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5548

Qy       5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5549 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5608

Qy       5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5609 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5668

Qy       5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5669 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5728

Qy       5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5729 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5788

Qy       5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5789 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5848
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Qy       5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5849 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5908

Qy       5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5909 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5968

Qy       5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5969 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6028

Qy       6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
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Db       6029 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6088

Qy       6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
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Db       6089 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6148

Qy       6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
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Db       6149 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6208

Qy       6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6209 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6268

Qy       6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6269 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6328

Qy       6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6329 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6388

Qy       6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
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Db       6389 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6448

Qy       6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6449 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6508

Qy       6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6509 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6568

Qy       6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6569 CTCTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6628

Qy       6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6629 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6688

Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6689 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6748

Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
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Db       6749 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6808

Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6809 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6868

Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6869 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6928

Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6929 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6988

Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6989 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7048

Qy       7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
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Db       7049 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7108

Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7109 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7168

Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
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Db       7169 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7228

Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
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Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
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Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
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Db       7349 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7408

Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
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Db       7409 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7468

Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
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Db       7469 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7528

Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7529 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7588

Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
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Db       7589 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7648

Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
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Db       7649 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7708

Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
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Db       7709 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7768

Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
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Db       7769 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7828

Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
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Db       7829 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7888

Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
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Db       7889 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7948

Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
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Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
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Db       8009 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8068

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Db       8069 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8128

Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
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Db       8129 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8188

Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
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Db       8189 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8248

Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
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Db       8249 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8308

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
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Db       8309 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8368

Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
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Db       8369 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8428

Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8429 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8488

Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
             |||||||||||| ||||||||||||||
Db       8489 CTGACTAATACCACAACACCACCACCT 8515


RESULT 7
ADL71910
ID   ADL71910 standard; cDNA; 17753 BP.
XX
AC   ADL71910;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Expression vector pCytTs-OPE.
XX
KW   Gene expression; vector; pCytTS; ss.
XX
OS   Alphavirus.
OS   Human herpesvirus 4.
OS   Chimeric.
XX
PN   WO2004018506-A2.
XX
PD   04-MAR-2004.
XX
PF   21-AUG-2003; 2003WO-EP009291.
XX
PR   22-AUG-2002; 2002US-0404928P.
PR   11-DEC-2002; 2002US-0432259P.
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI   Ivanova L,  Renner WA,  Saudan P;
XX
DR   WPI; 2004-226795/21.
XX
PT   New nucleic acid molecule comprising first, second and third
PT   polynucleotide elements, useful for regulating the expression of a
PT   polypeptide or an untranslated RNA molecule.
XX
PS   Example 2; SEQ ID NO 22; 112pp; English.
XX
CC   The present sequence is that of expression vector pCytTs-OPE. A claimed
CC   nucleic acid molecule comprises: (A) a first polynucleotide element which
CC   encodes an RNA molecule comprising (a) at least one cis-acting sequence
CC   element, (b) a first nucleotide sequence comprising a first open reading
CC   frame, the first open reading frame having a nucleotide sequence encoding
CC   an RNA-dependent RNA polymerase, and (c) at least one second nucleotide
CC   sequence comprising (i) a second open reading frame (S1) encoding a
CC   polypeptide, (ii) a nucleotide sequence complementary to all or a part of
CC   the second open reading frame (S1) and (iii) a nucleotide sequence
CC   encoding an untranslated RNA molecule or its complement, where the second
CC   nucleotide sequence is operably linked to a promoter which is recognised
CC   by the RNA-dependent RNA polymerase; (B) a second polynucleotide element
CC   comprising an origin of replication; and (C) a third polynucleotide
CC   element encoding a replication initiation factor capable of recognising
CC   the origin of replication. The nucleic acid molecule, expression systems
CC   and vector systems of the invention allow the production of polypeptides
CC   and untranslated RNA molecules in host cells. In a specific embodiment,
CC   the invention includes the combination of a herpesvirus mini-replicon
CC   unit, e.g. the cis-acting replication origin oriP and replication
CC   initiation factor EBNA1 from Epstein Barr virus, with pCysTS ADL71889,
CC   creating pCytTs-ORE. Due to the presence of OriP and EBNA1, the novel
CC   vector is maintained episomally in the form of several DNA copies in cell
CC   nuclei. These multiple DNA copies may be transcribed from a Rous sarcoma
CC   virus or cytomegalovirus promoter into pCysTS RNA replicons, but remain
CC   inactive unless cells are shifted to a certain temperature. Only after
CC   temperature induction does replicon replication occur, followed by RNA
CC   accumulation and translation in the cell cytoplasm, and production of the
CC   polypeptide of interest.
XX
SQ   Sequence 17753 BP; 4502 A; 4902 C; 4209 G; 4140 T; 0 U; 0 Other;

  Query Match           89.7%;  Score 7657.2;  DB 12;  Length 17753;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7642;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 928

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
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Db        929 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 988

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
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Db        989 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1048

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db       1169 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATATGCCAGTA 1228

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1229 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1288

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1289 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1348

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1349 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1408

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1409 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1468
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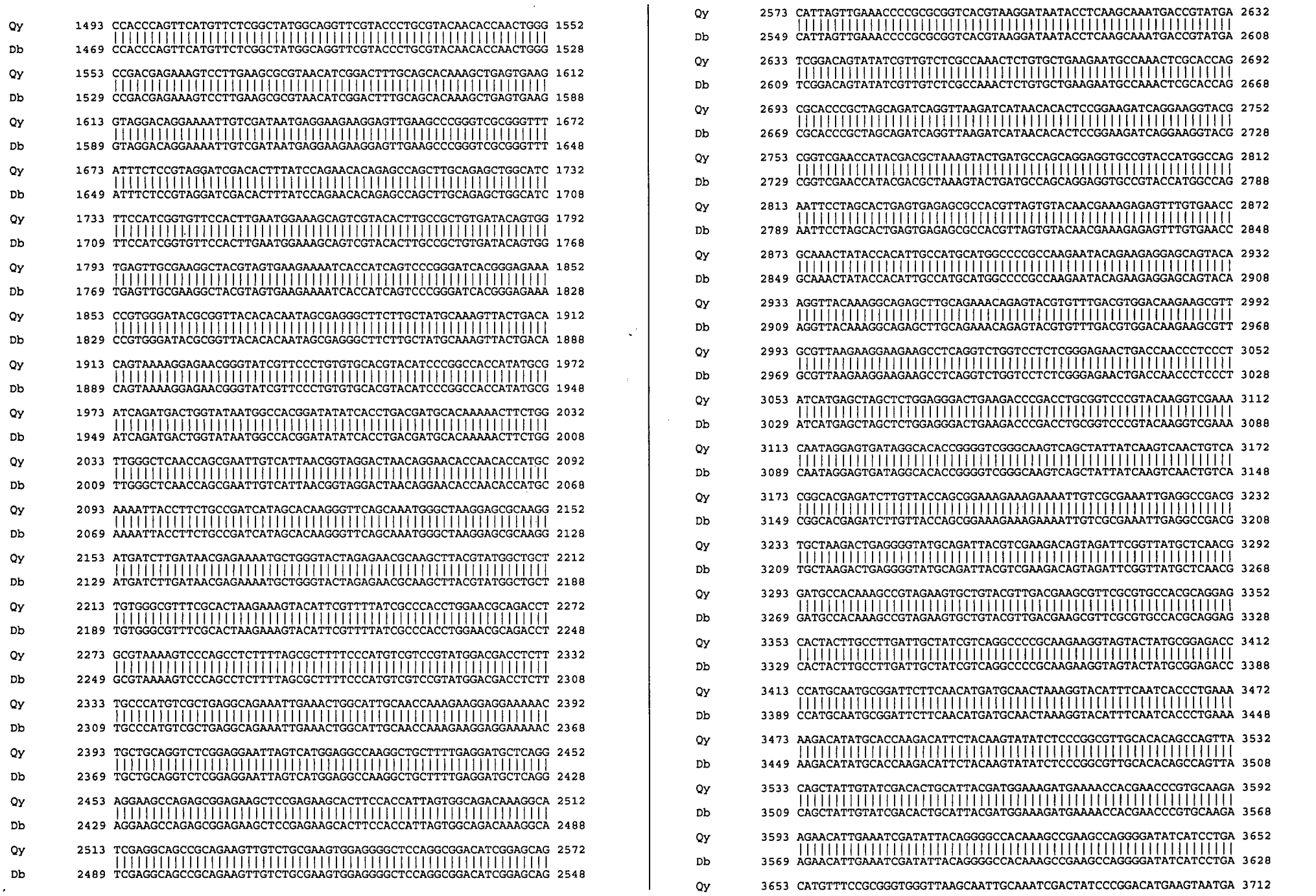
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Db 1469 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1528
Qy 1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
Db 1529 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1588
Qy 1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
Db 1589 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1648
Qy 1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
Db 1649 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1708
Qy 1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
Db 1709 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1768
Qy 1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
Db 1769 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1828
Qy 1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
Db 1829 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1888
Qy 1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
Db 1889 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1948
Qy 1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
Db 1949 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2008
Qy 2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
Db 2009 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2068
Qy 2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
Db 2069 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2128
Qy 2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
Db 2129 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2188
Qy 2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
Db 2189 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2248
Qy 2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
Db 2249 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2308
Qy 2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
Db 2309 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2368
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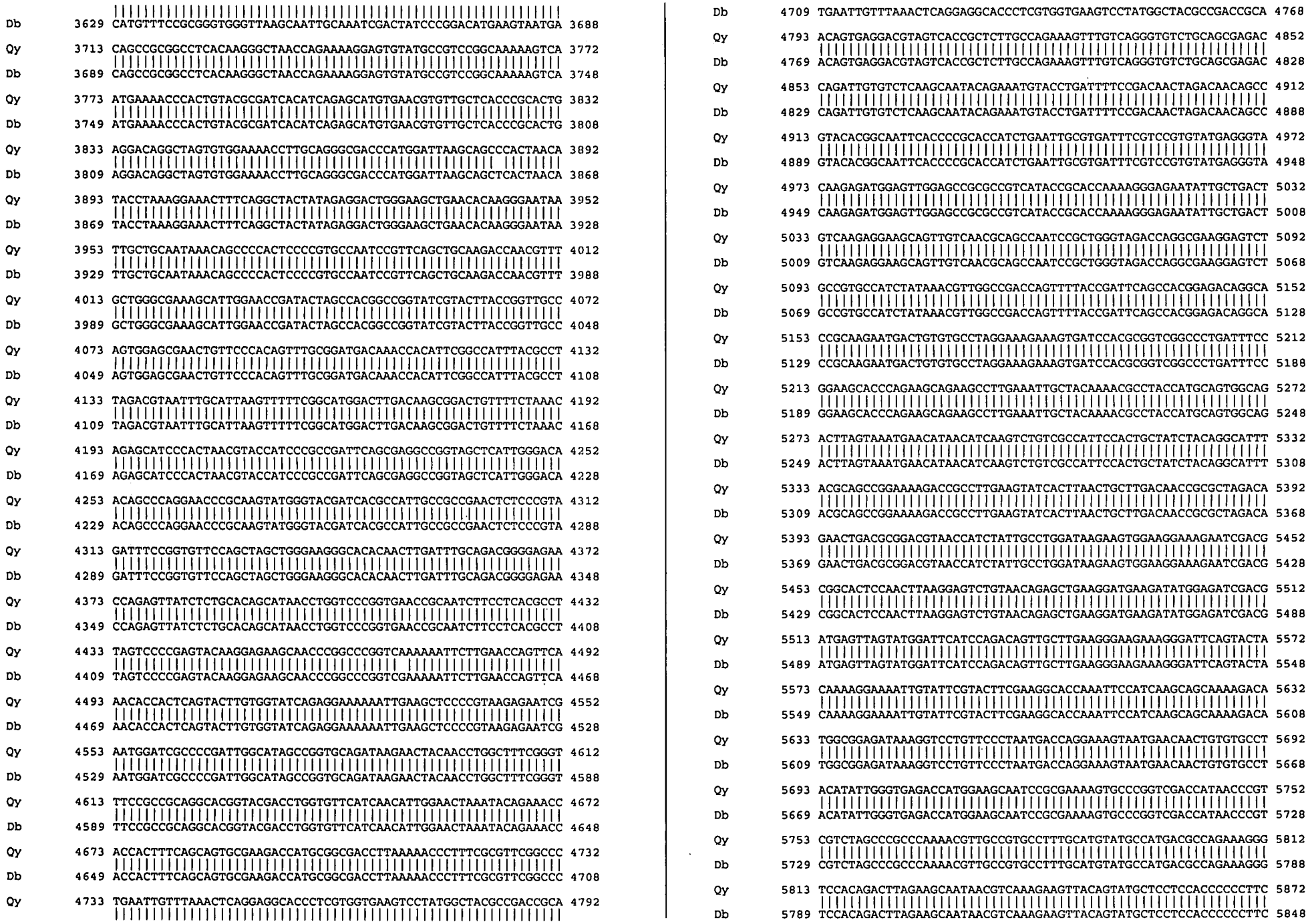
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Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
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Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
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Db       8489 CTGACTAATACCACAACACCACCACCT 8515
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RESULT 8
AAX77354
ID AAX77354 standard; DNA; 9951 BP.
XX
AC AAX77354;
XX
DT 09-AUG-1999 (first entry)
XX
DE Polynucleotide sequence of pSinRep 5.
XX
KW Nucleic acid identification; exogenous protein; gene sorting;
KW growth factor; membrane receptor; sindbis virus; ss.
XX
OS Synthetic.
XX
PN WO9925876-A1.
XX
PD 27-MAY-1999.
XX
PF 17-NOV-1998; 98WO-US024520.
XX
PR 17-NOV-1997; 97US-00972218.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
XX
PI Bailey JE, Renner WA, Orberger GH, Koller D;
XX
DR WPI; 1999-357620/30.
XX
PT Isolating genes encoding proteins with selected properties, useful for
PT identifying therapeutic agents or targets.
XX
PS Disclosure; Fig 11A-C; 136pp; English.
XX
CC The invention relates to the identification of a recombinant nucleic acid
CC encoding an exogenous protein having a selected property. The method
CC comprises preparing a population of eukaryotic host cells, culturing the
CC cells under suitable conditions and identifying cells that contain the
CC recombinant nucleic acid. The method is used to sort genes according to
CC the type of proteins they express, and also to identify new ligand/
CC receptor interactions. Typical applications of the nucleic acid and the
CC exogenous protein are in isolation of new growth factors, cytokines,
CC membrane receptors, cytoplasmic, organelle or nuclear proteins, all of
CC which may be useful as therapeutic agents or therapeutic targets, e.g.
CC apoptosis-promoting or tumour suppressing proteins, regulators of cell
CC proliferation or metabolic processes etc. The protein can also be used to
CC screen for specific modulators. The nucleic acid can also be used as
CC sources of therapeutic antisense or ribozyme sequences. The method allows
CC the protein (rather than a partial DNA sequence) to be isolated and,
CC since a wide range of cells can be used, they can be expressed with the
CC correct glycosylation pattern
XX
SQ Sequence 9951 BP; 2852 A; 2461 C; 2464 G; 2174 T; 0 U; 0 Other;

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  Query Match             89.4%;  Score 7637.4;  DB 2;  Length 9951;
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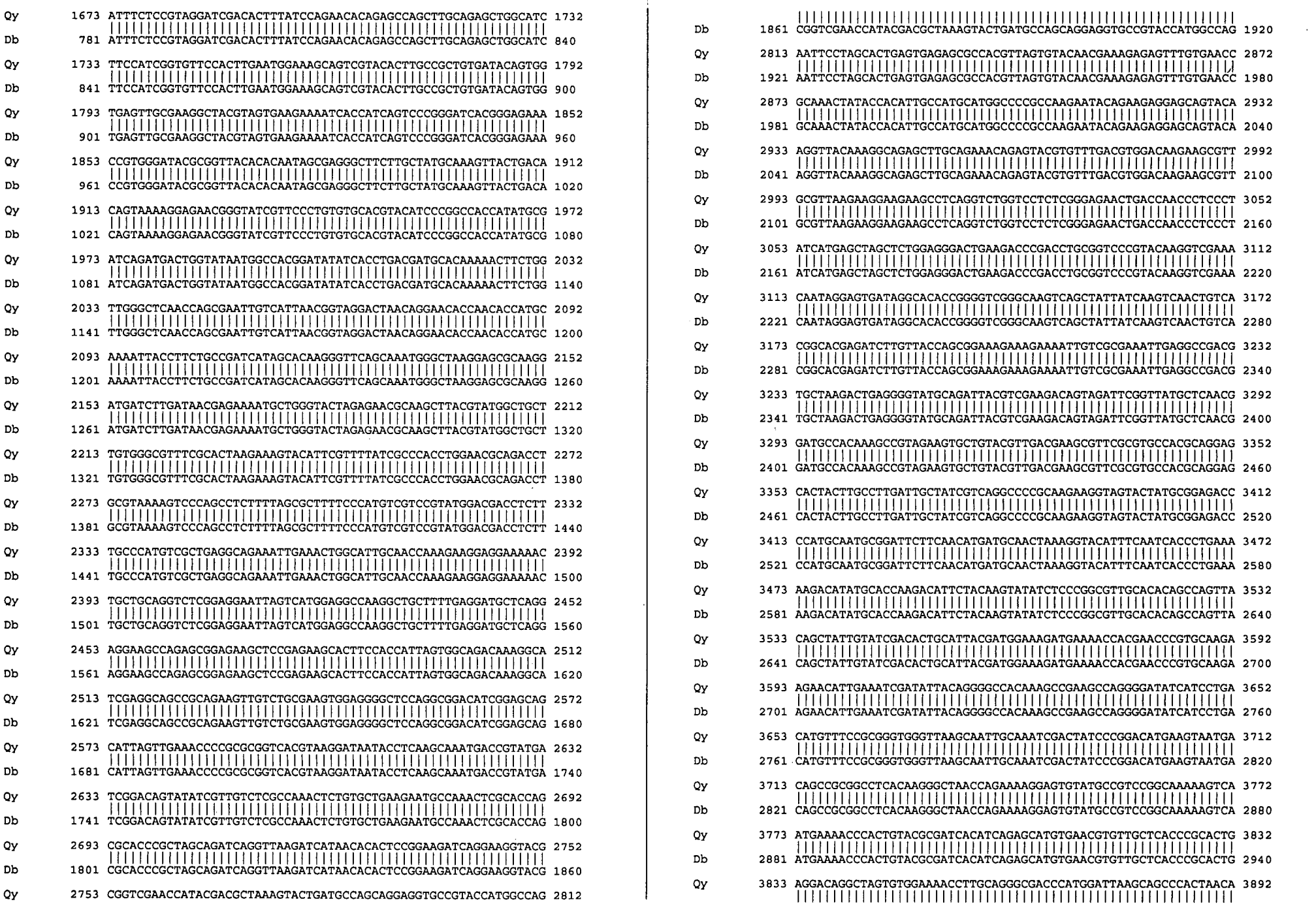
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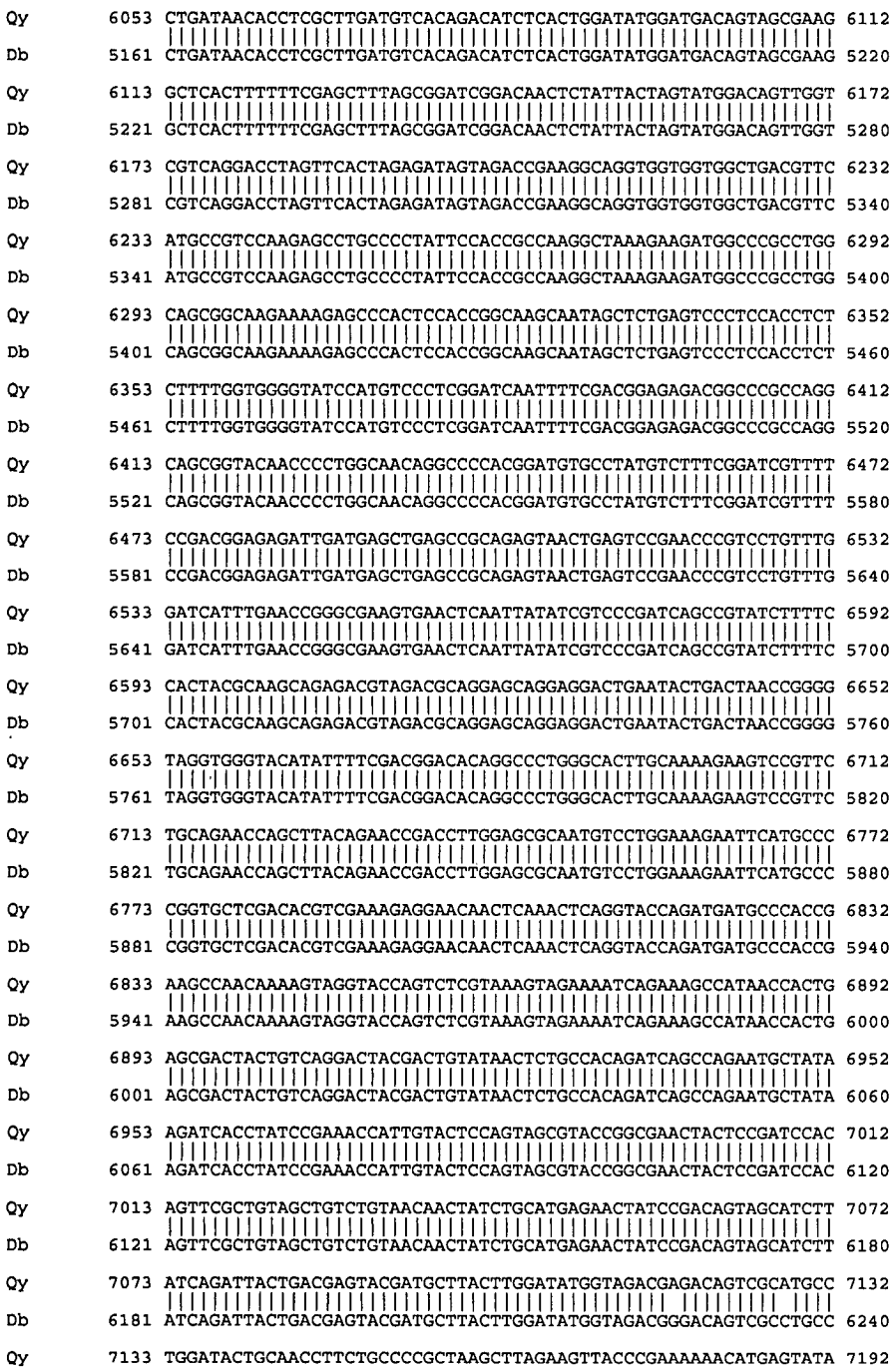
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RESULT 9
AAA90386
ID   AAA90386 standard; DNA; 9951 BP.
XX
AC   AAA90386;
XX
DT   10-JAN-2001  (first entry)
XX
DE   Sindbis expression vector pSinRep5 DNA sequence.
XX
KW   Nucleic acid identification; exogenous protein; drug screening;
KW   recombinant expression; pSinRep5; mammalian expression system; cyclic;
KW   circular; ds.
XX
OS   Synthetic.
OS   Sindbis virus.
XX
PN   JP2000189173-A.
XX
PD   11-JUL-2000.
XX
PF   23-AUG-1999;   99JP-00236220.
XX
PR   17-NOV-1998;   98US-00193707.
PR   17-NOV-1998;   98WO-US024520.
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
XX
DR   WPI; 2000-551637/51.
XX
PT   Identifying a recombinant nucleic acid to identify and isolate various
PT   cellular proteins, comprises culturing a composition comprising
PT   eukaryotic host cells and identifying a cell comprising recombinant
PT   nucleic acid.
XX
PS   Example 7; Fig 11A-C; 56pp; Japanese.
XX
CC   The invention relates to the identification of a recombinant nucleic acid
CC   encoding an exogenous protein having a selected property.The method
CC   comprises preparing populations of eukaryotic host cells, where each cell
CC   comprises an expression vector encoding a different exogenous protein.
CC   The host cells are cultured under suitable conditions and the nucleic
CC   acid which encodes the exogenous protein is identified. The method is
CC   useful for the identification and isolation of proteins with a selected
CC   property. Typical applications of the nucleic acid and the exogenous
CC   protein are in isolation of new growth factors, cytokines, membrane
CC   receptors, cytoplasmic, organelle or nuclear proteins, all of which may
CC   be useful as therapeutic agents or therapeutic targets, e.g., pro-
CC   apoptotic or tumour suppressing proteins, regulators of cell
CC   proliferation or of metabolic processes. The protein can also be used to
CC   screen for ligands and specific modulators of activity. The method of the
CC   invention allows the direct cloning of full length cDNAs in one step. It
CC   facilitates direct expression of the protein without the need to perform
CC   further procedures such as subcloning and establishment of a cell line
CC   for protein production. The method allows a protein of interest (rather
CC   than a partial DNA sequence) to be isolated and, since a wide range of
CC   cell types can be used, they can be expressed in a correctly folded and
CC   glycosylated form. The present sequence represents the Sindbis expression
CC   vector pSinRep5 which was used in the exemplifications of the invention.
CC   This patent is related to WO9925876
XX
SQ   Sequence 9951 BP; 2852 A; 2461 C; 2464 G; 2174 T; 0 U; 0 Other;

  Query Match             89.4%;  Score 7637.4;  DB 3;  Length 9951;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7641;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

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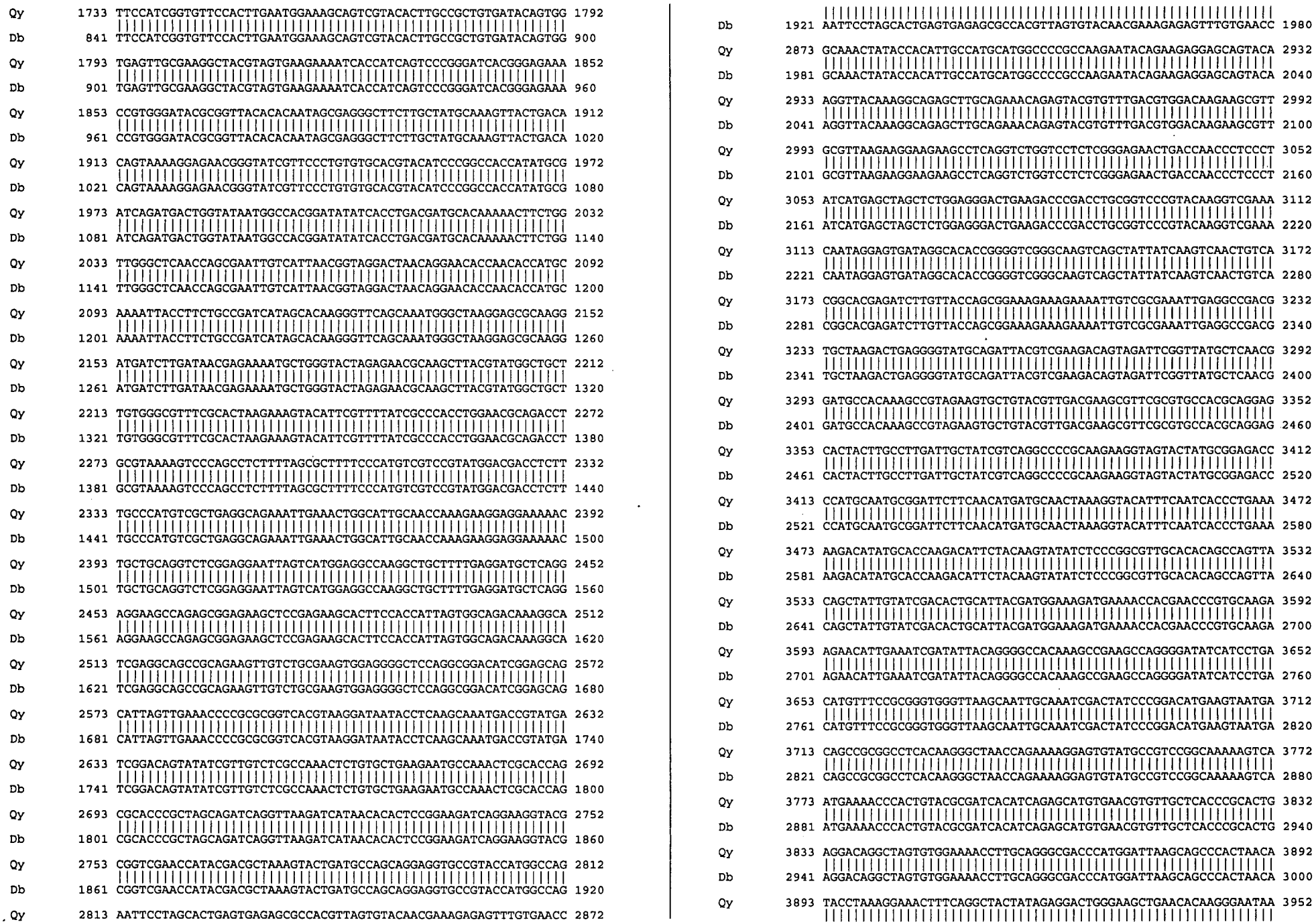
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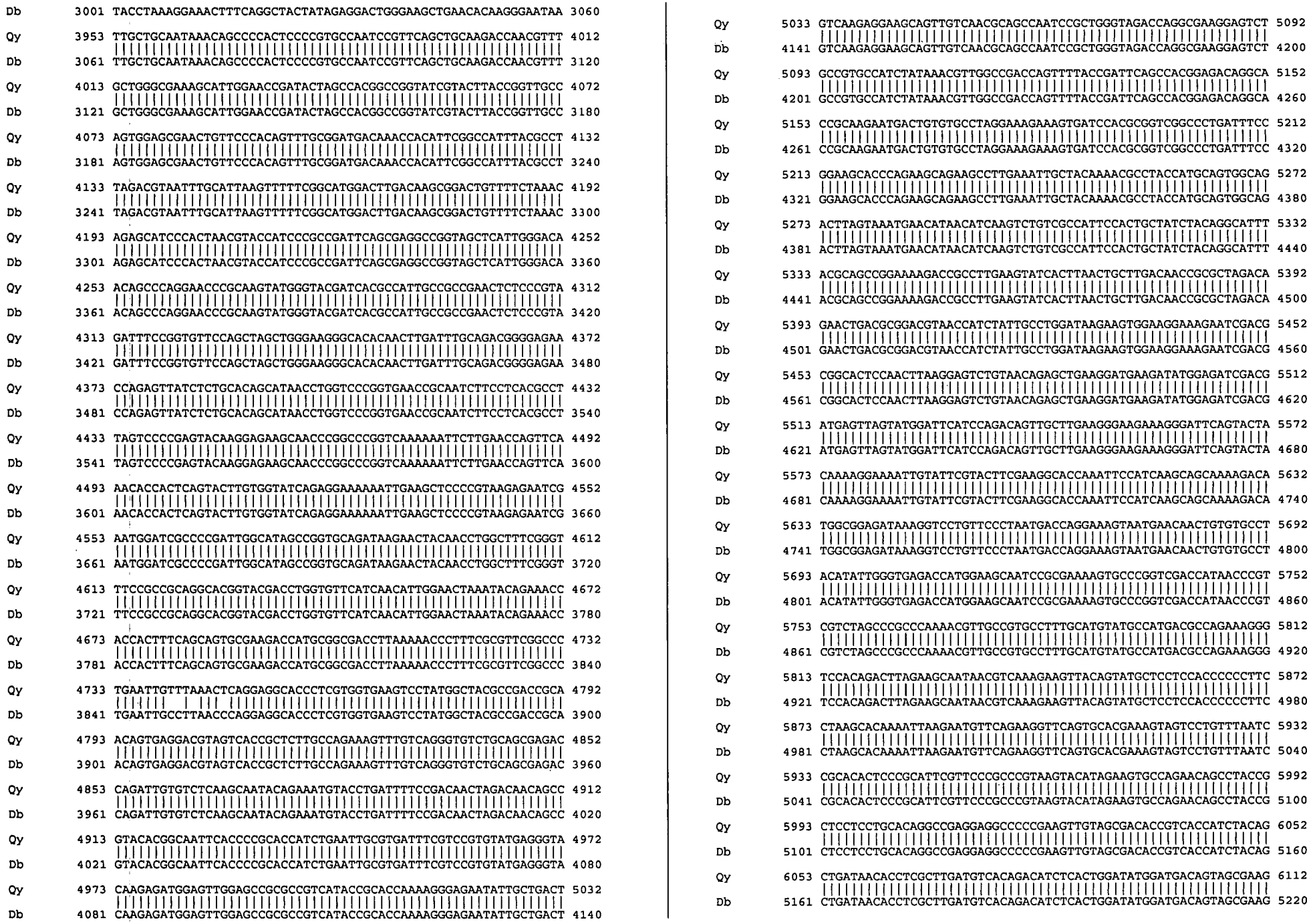
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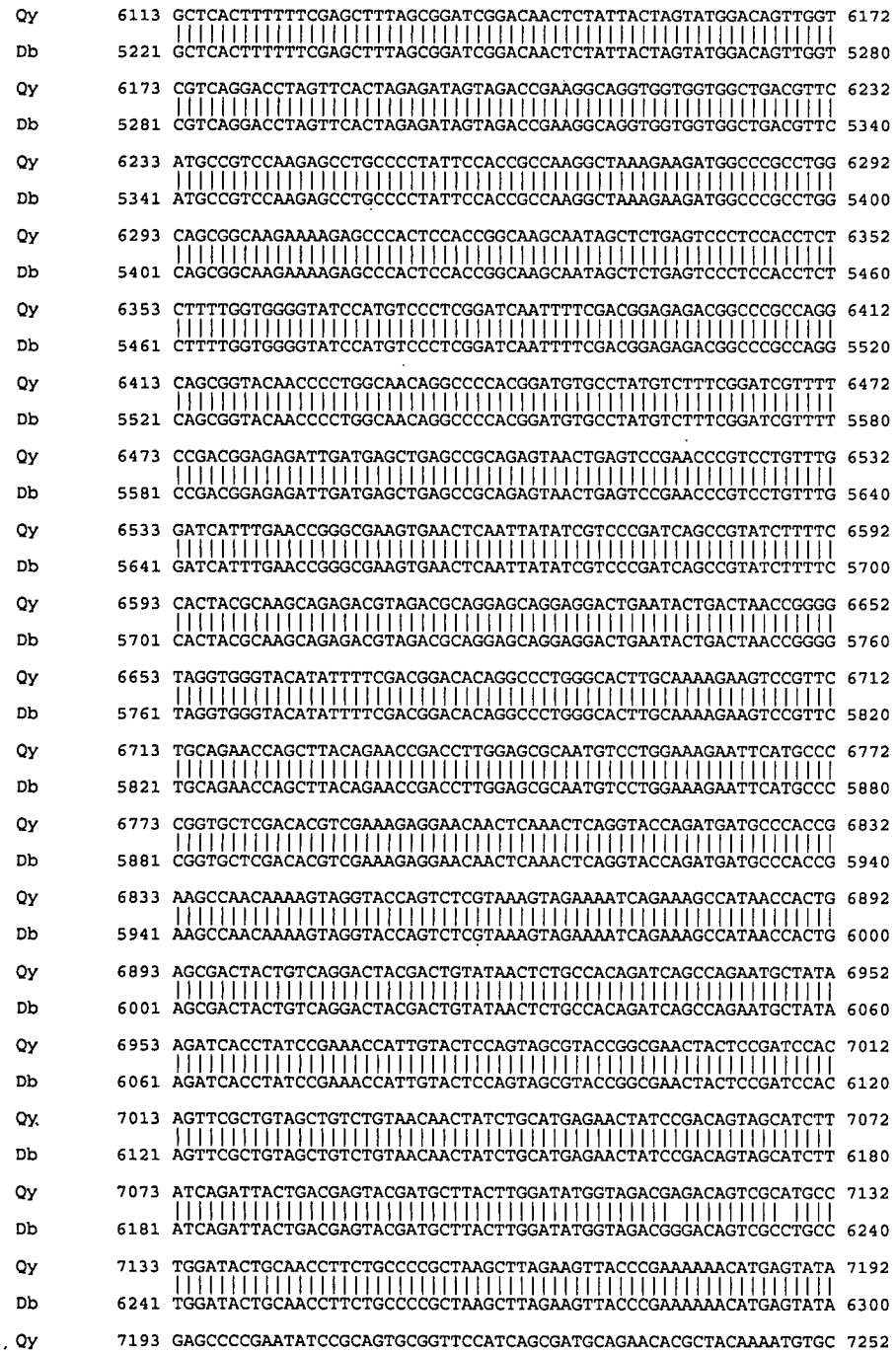
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RESULT 10
AAD04742
ID   AAD04742 standard; DNA; 9951 BP.
XX
AC   AAD04742;
XX
DT   17-JUL-2001  (first entry)
XX
DE   Alphaviral vector pSinRep5 DNA.
XX
KW   pSinRep5; alphaviral vector; vaccine; therapy; cancer; antiparasitic;
KW   antimalarial; anticancer; anti-HIV; antiviral; infectious disease;
KW   Human immunodeficiency virus; HIV; influenza; passive immunisation;
KW   carcinoma; liver; skin; stomach; ovarian tumour; ds.
XX
OS   Synthetic.
XX
PN   WO200130989-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-IB001557.
XX
PR   27-OCT-1999;  99US-0161796P.
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA   (RENN/) RENNER W A.
PA   (NIEB/) NIEBA L.
XX
PI   Renner WA, Nieba L;
XX
DR   WPI; 2001-308631/32.
XX
PT   Preparing alphaviral vectors with mutations in a selected gene, for use
PT   as vaccines, particularly against pathogens that mutate rapidly,
PT   comprises replicating in the presence of a nucleoside analog.
XX
PS   Claim 4; Fig 4; 103pp; English.
XX
CC   The present invention relates to a method for preparing viral vectors
CC   which comprises inserting a gene of interest into an alphaviral vector
CC   such as pCYTts, pSinRep5 and replicating the vector in the presence of
CC   alphaviral replicase and nucleoside analogues (5'azacytidine (AZT), FU-
CC   5' fluorouridine) to produce a modified gene of interest. The replication
CC   is repeated until the modified gene in 90 % of the vector population
CC   contain a mutation in the modified gene which is 90-99 % identical with
CC   the gene of interest. The vector populations are used in vaccines for
CC   treatment or prevention of a wide variety of infectious diseases (viral
CC   or parasitic, e.g. human immuno deficiency virus (HIV), influenza,
CC   Trypanosoma or Plasmodium) and cancers such as liver carcinoma, stomach
CC   carcinoma, skin carcinoma and ovarian tumours. Vaccines containing the
CC   mutant populations will therefore be effective against viral escape
CC   mutants. Mutagenesis in a eukaryotic cell ensures that expressed proteins
CC   are correctly glycosylated. Antisera raised against the vaccines can be
CC   used for passive immunisation. The present DNA sequence is an alphaviral
CC   vector pSinRep5. pSinRep5 contains nucleic acid which encodes a wild-type
CC   alphaviral replicase. Thus, this replicase in cytopathic and eukaryotic
CC   cells which express it will generally become non-viable within 24 hours
CC   after initiation of expression
XX
SQ   Sequence 9951 BP; 2852 A; 2460 C; 2465 G; 2174 T; 0 U; 0 Other;

  Query Match             89.4%;  Score 7637.4;  DB 4;  Length 9951;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7641;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

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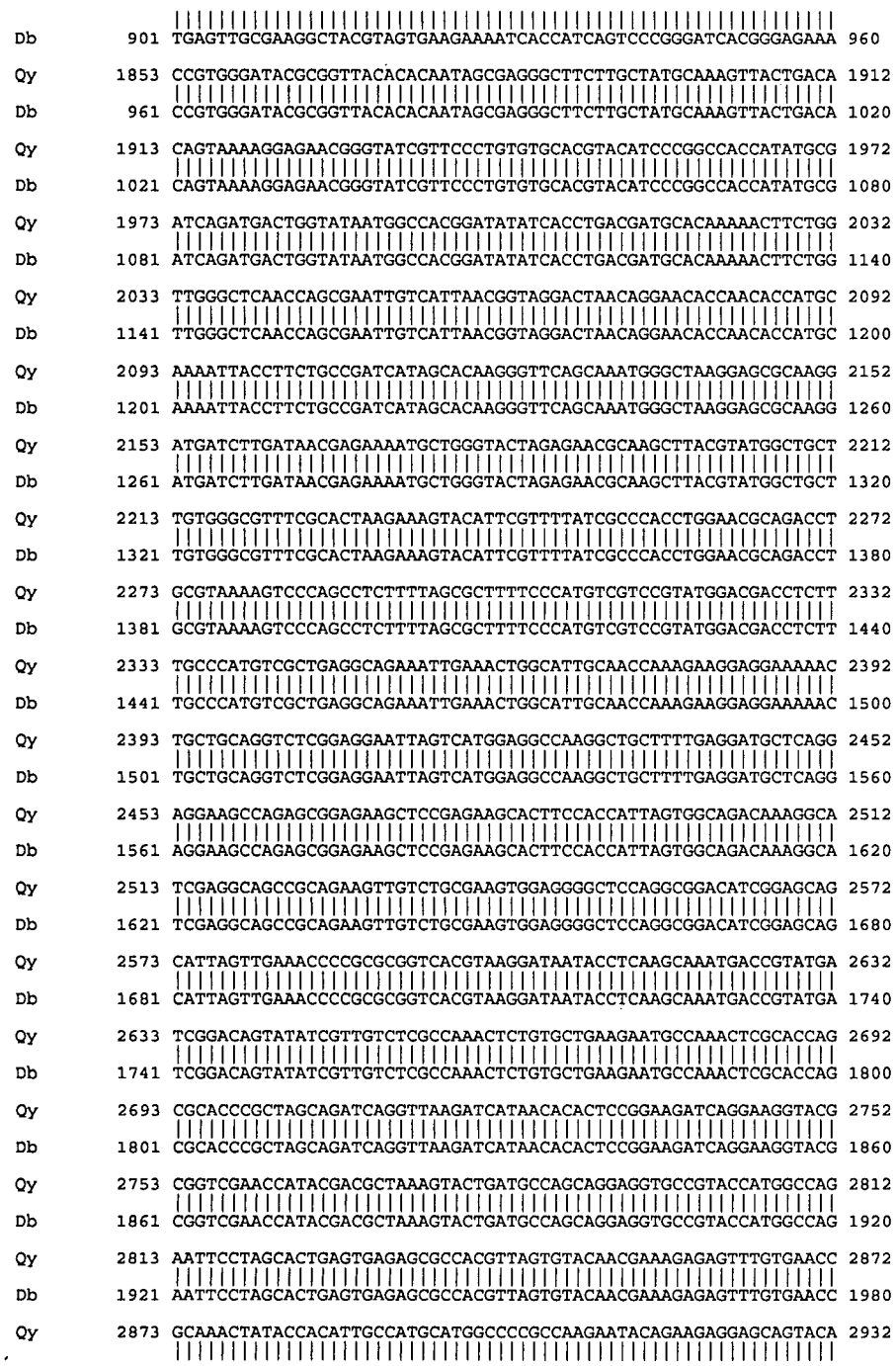
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Qy 2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
Db 1741 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 1800
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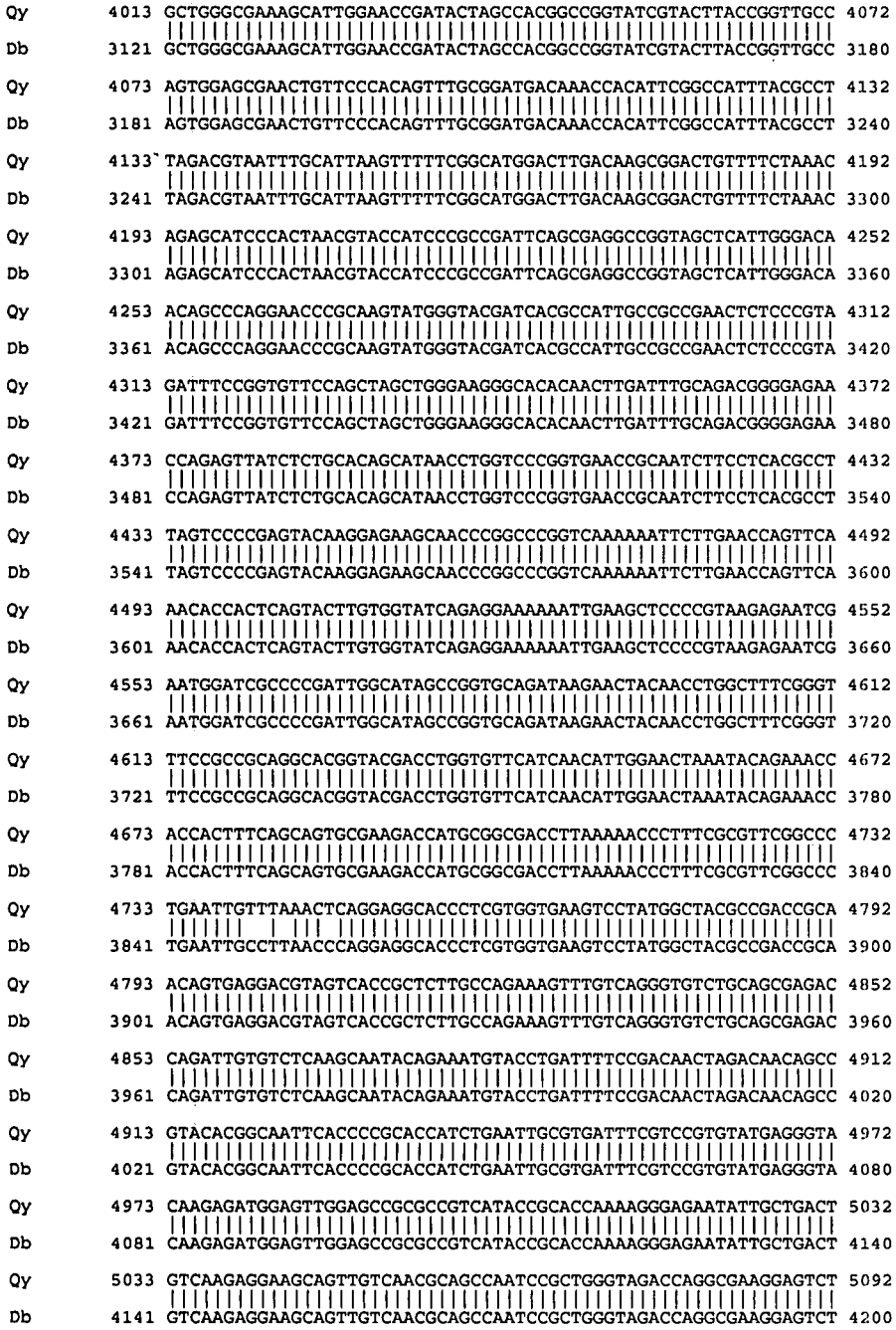
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Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
Db       7261 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 7320
Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
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Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
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Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
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Db       7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 7620

Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
             |||||||||||||||||||||||||||
Db       7621 CTGACTAATACTACAACACCACCACCT 7647


RESULT 11
ABN86686
ID   ABN86686 standard; DNA; 9951 BP.
XX
AC   ABN86686;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Nucleotide sequence of a SINrep5 self replicating replicon.
XX
KW   Major histocompatibility complex; MHC; antigen presenting cell; APC;
KW   antigen; cytostatic; virucide; gene therapy; CD8; vaccine; therapeutic;
KW   cancer; viral infection; ds.
XX
OS   Synthetic.
XX
PN   WO200261113-A2.
XX
PD   08-AUG-2002.
XX
PF   01-FEB-2002; 2002WO-US002598.
XX
PR   01-FEB-2001; 2001US-0265334P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Wu T,  Hung C;
XX
DR   WPI; 2002-619261/66.
XX
PT   Nucleic acid molecule encoding a fusion polypeptide that promotes
PT   processing via the Major Histocompatibility Complex class I pathway
PT   and/or promotes activity of an antigen presenting cell, useful as vaccine
PT   for cancer and viral infections.
XX
PS   Claim 27; Page 23-25; 127pp; English.
XX
CC   The invention relates to a new nucleic acid molecule (I) encoding a
CC   fusion polypeptide useful as a vaccine composition. (I) comprises a first
CC   nucleic acid sequence encoding a first polypeptide or peptide that
CC   promotes processing via the Major Histocompatibility Complex (MHC) class
CC   I pathway (MHC-I-PP) and/or promotes development or activity of an
CC   antigen presenting cell (APC). The second nucleic acid sequence is linked
CC   in frame to the first nucleic acid sequence or to a linker nucleic acid
CC   sequence and encodes an antigenic polypeptide or peptide. The methods and
CC   compositions of the present invention are useful as therapeutic vaccine
CC   for cancer and for major viral infections, such as hepatoma and cervical
CC   cancer, that cause morbidity and mortality. They can also be used in
CC   treating animal diseases, such as equine herpesvirus, bovine viruses,
CC   Marek's disease, retroviral and lentiviral diseases and rabies, in the
CC   veterinary medicine context. The present sequence represents the
CC   nucleotide sequence of a SINrep5 self replicating replicon
XX
SQ   Sequence 9951 BP; 2852 A; 2460 C; 2465 G; 2174 T; 0 U; 0 Other;

  Query Match           89.4%;  Score 7637.4;  DB 6;  Length 9951;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 7641;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
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Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
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Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
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Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
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Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
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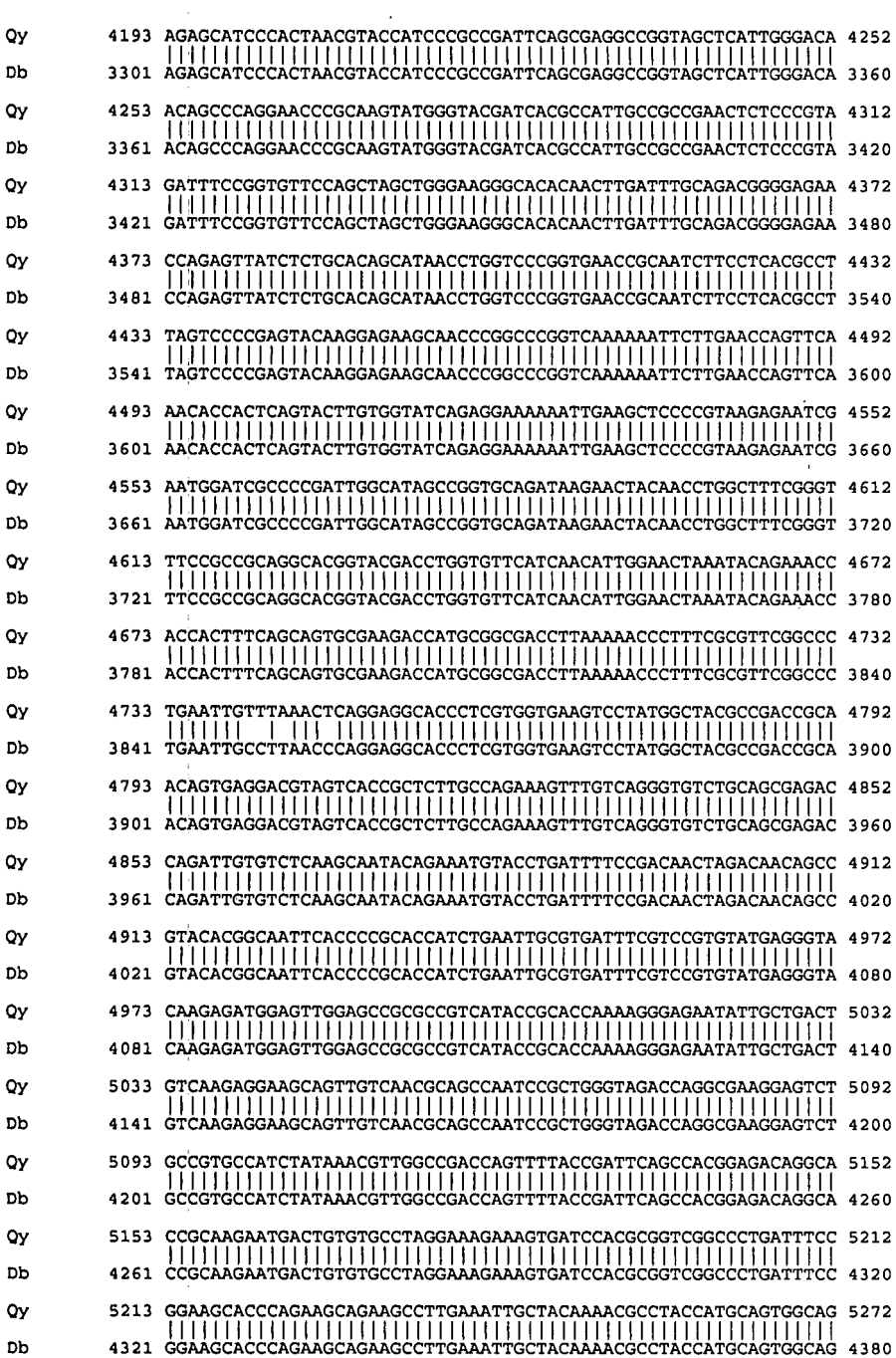
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Qy       7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
Db       6181 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGGGACAGTCGCCTGCC 6240
Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
Db       6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 6300
Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
Db       6301 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 6360
Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
Db       6361 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 6420
Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
Db       6421 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 6480
Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
Db       6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540
Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
Db       6541 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 6600
Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
Db       6601 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 6660
Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
Db       6661 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 6720
Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
Db       6721 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 6780
Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
Db       6781 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 6840
Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
Db       6841 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 6900
Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
Db       6901 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 6960
Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
Db       6961 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7020
Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
Db       7021 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7080
Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
Db       7081 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 7140
Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
Db       7141 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 7200
Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
Db       7201 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 7260
Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
Db       7261 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 7320
Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
Db       7321 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 7380
Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
Db       7381 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 7440
Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
Db       7441 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 7500
Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
Db       7501 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 7560
Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
Db       7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 7620
Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
Db       7621 CTGACTAATACTACAACACCACCACCT 7647
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RESULT 12
ABV73174
ID   ABV73174 standard; DNA; 9951 BP.
XX
AC   ABV73174;
XX
DT   08-JAN-2003  (first entry)
XX
DE   Nucleotide sequence of Sinrep5 self replicating replicon.
XX
KW   Immunogenicity; cytostatic; virucide; protozoacide; antibacterial; CTL;
KW   hepatotropic; anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; ds.
XX
OS   Sindbis virus.
XX
PN   WO200274920-A2.
XX
PD   26-SEP-2002.
XX
PF   18-MAR-2002; 2002WO-US008033.
XX
PR   16-MAR-2001; 2001US-0276854P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Wu T,  Hung C;
XX
DR   WPI; 2002-740856/80.
XX
PT   New nucleic acid molecule encoding an antigenic fusion polypeptide useful
PT   as vaccines for enhancing or inducing immune responses, primarily
PT   cytotoxic T lymphocytes (CTL) responses to specific antigens such as
PT   tumor or viral antigens.
XX
PS   Disclosure; Page 56-58; 93pp; English.
XX
CC   The invention relates to a nucleic acid molecule that encodes a fusion
CC   polypeptide, comprising a first nucleic acid sequence encoding a
CC   polypeptide that comprises at least one immunogenicity-potentiating
CC   polypeptide, optionally, fused in frame with the nucleic acid, a linker
CC   nucleic acid encoding a linker peptide, and a nucleic acid that is linked
CC   in frame to them, and that encodes an antigenic peptide or polypeptide.
CC   The nucleic acid molecule, polypeptides and vectors are useful as
CC   vaccines for enhancing immune responses, primarily cytotoxic T
CC   lymphocytes (CTL) responses to specific antigens such as tumour or viral
CC   antigens, and for inhibiting growth or preventing re-growth of a tumour.
CC   The packaging cell line is useful for generating alphavirus replicon
CC   particles without contamination from replicon-competent virus. The
CC   pathogenic organisms include viruses such as human papilloma virus (HPV),
CC   hepatitis B virus, hepatitis C virus, human immunodeficiency virus,
CC   Epstein Barr virus and herpes simplex virus, intracellular parasites such
CC   as malaria, and bacteria that grow intracellularly such as mycobacteria
CC   and listeria. The present sequence represents the nucleotide sequence of
CC   the sindbis virus RNA replicon vector Sinrep5, a self replicating
CC   replicon
XX
SQ   Sequence 9951 BP; 2852 A; 2460 C; 2465 G; 2174 T; 0 U; 0 Other;

  Query Match             89.4%;  Score 7637.4;  DB 6;  Length 9951;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7641;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140

Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 1200

Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
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Db       1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260
Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
Db       1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320
Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
Db       1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380
Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
Db       1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440
Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
Db       1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500
Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
Db       1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560
Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
Db       1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620
Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
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Db       1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740
Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
Db       1741 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 1800
Qy       2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
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Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
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Qy       2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
Db       1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980
Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
Db       1981 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2040
Qy       2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
Db       2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100
Qy       2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
Db       2101 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 2160
Qy       3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
Db       2161 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 2220
Qy       3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
Db       2221 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280
Qy       3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
Db       2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340

Qy       3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
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Db       2401 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 2460
Qy       3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
Db       2461 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 2520
Qy       3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
Db       2521 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 2580
Qy       3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
Db       2581 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 2640
Qy       3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
Db       2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700
Qy       3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
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Db       2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820
Qy       3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
Db       2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880
Qy       3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
Db       2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940
Qy       3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
Db       2941 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3000
Qy       3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
Db       3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060
Qy       3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
Db       3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120
Qy       4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
Db       3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180
Qy       4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
Db       3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240
Qy       4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
Db       3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 3300
Qy       4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
Db       3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360
Qy       4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
Db       3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420
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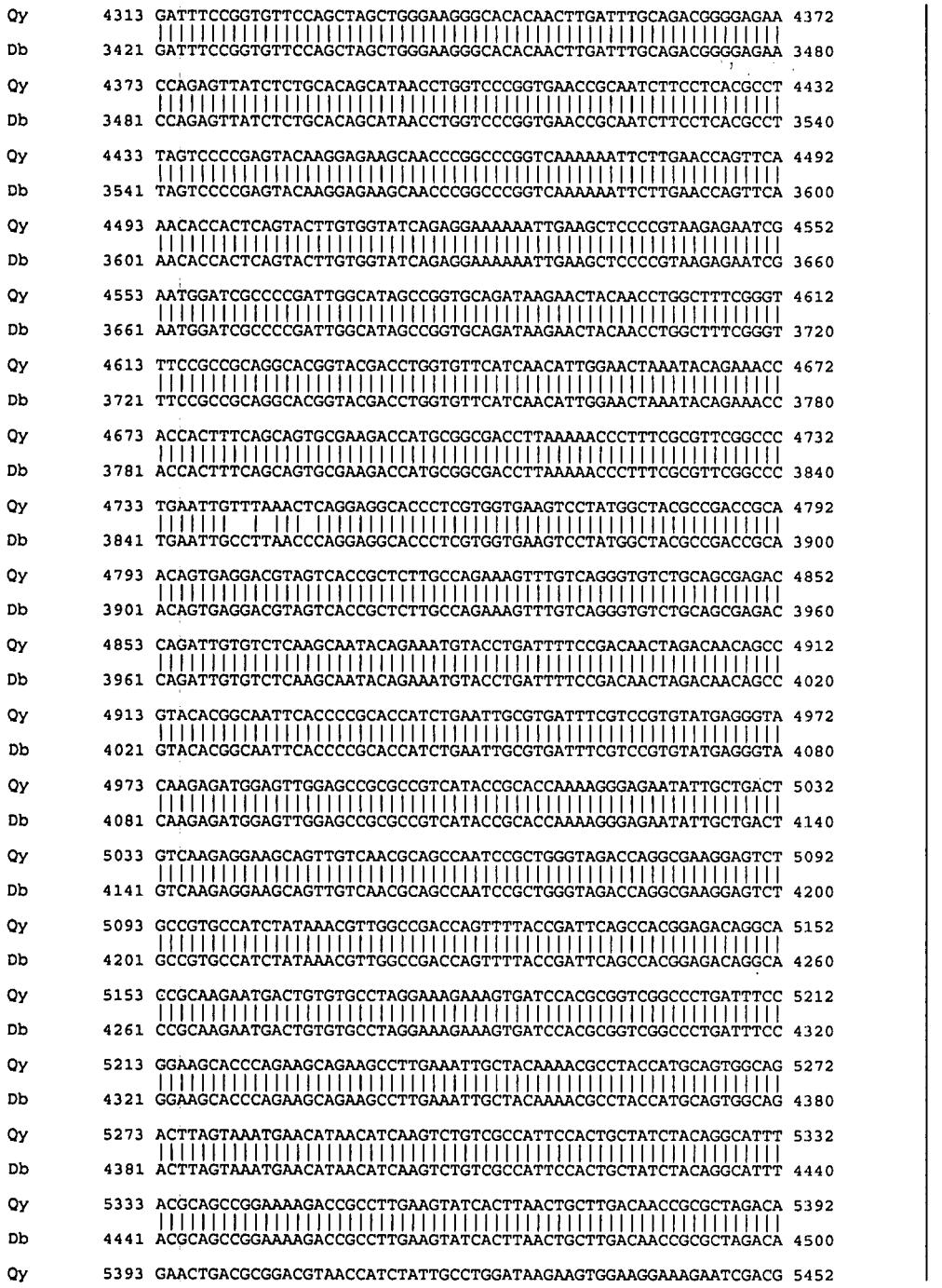
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Db 3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480
Qy 4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
Db 3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540
Qy 4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
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Db 3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780
Qy 4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
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Qy 4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
Db 3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900
Qy 4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
Db 3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960
Qy 4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
Db 3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020
Qy 4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
Db 4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080
Qy 4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
Db 4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140
Qy 5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
Db 4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200
Qy 5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
Db 4201 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 4260
Qy 5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
Db 4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320
Qy 5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
Db 4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380
Qy 5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
Db 4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440
Qy 5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
Db 4441 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 4500
Qy 5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
Db 4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560
Qy 5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
Db 4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620
Qy 5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
Db 4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680
Qy 5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
Db 4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740
Qy 5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
Db 4741 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 4800
Qy 5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
Db 4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860
Qy 5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
Db 4861 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 4920
Qy 5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
Db 4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980
Qy 5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
Db 4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040
Qy 5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
Db 5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100
Qy 5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
Db 5101 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 5160
Qy 6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
Db 5161 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 5220
Qy 6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
Db 5221 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280
Qy 6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
Db 5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340
Qy 6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
Db 5341 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 5400
Qy 6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
Db 5401 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 5460
Qy 6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
Db 5461 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 5520
Qy 6413 CAGCGGTACAACCCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
Db 5521 CAGCGGTACAACCCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 5580
Qy 6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532

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Db       5581 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 5640
Qy       6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5641 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 5700
Qy       6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 5760
Qy       6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 5820
Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 5880
Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 5940
Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000
Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6060
Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6120
Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 6180
Qy       7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
             |||||||||||||||||||||||||||||||||||||||||||| |||||||| ||||
Db       6181 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGGGACAGTCGCCTGCC 6240
Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 6300
Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 6360
Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 6420
Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6421 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 6480
Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540
Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6541 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 6600
Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6601 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 6660
Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6661 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 6720

Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6721 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 6780
Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6781 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 6840
Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6841 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 6900
Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6901 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 6960
Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6961 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7020
Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7021 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7080
Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 7140
Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7141 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 7200
Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7201 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 7260
Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 7320
Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 7380
Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 7440
Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7441 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 7500
Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7501 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 7560
Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 7620
Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
             ||||||||||||||||||||||||||||
Db       7621 CTGACTAATACTACAACACCACCACCT 7647
```

RESULT 13
ABN86689
ID ABN86689 standard; DNA; 12110 BP.
XX
AC ABN86689;
XX
DT 05-NOV-2002 (first entry)

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XX
DE   Nucleotide sequence of vector Sinrep5-E7-Hsp70.
XX
KW   Major histocompatibility complex; MHC; antigen presenting cell; APC;
KW   antigen; cytostatic; virucide; gene therapy; CD8; vaccine; therapeutic;
KW   cancer; viral infection; HPV; E7; heat shock protein 70; Hsp70; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    7715. .9819
FT                   /*tag= a
FT                   /note= "E7-Hsp70 fusion sequence"
XX
PN   WO200261113-A2.
XX
PD   08-AUG-2002.
XX
PF   01-FEB-2002; 2002WO-US002598.
XX
PR   01-FEB-2001; 2001US-0265334P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Wu T,  Hung C;
XX
DR   WPI; 2002-619261/66.
XX
PT   Nucleic acid molecule encoding a fusion polypeptide that promotes
PT   processing via the Major Histocompatibility Complex class I pathway
PT   and/or promotes activity of an antigen presenting cell, useful as vaccine
PT   for cancer and viral infections.
XX
PS   Claim 36; Page 30-33; 127pp; English.
XX
CC   The invention relates to a new nucleic acid molecule (I) encoding a
CC   fusion polypeptide useful as a vaccine composition. (I) comprises a first
CC   nucleic acid sequence encoding a first polypeptide or peptide that
CC   promotes processing via the Major Histocompatibility Complex (MHC) class
CC   I pathway (MHC-I-PP) and/or promotes development or activity of an
CC   antigen presenting cell (APC). The second nucleic acid sequence is linked
CC   in frame to the first nucleic acid sequence or to a linker nucleic acid
CC   sequence and encodes an antigenic polypeptide or peptide. The methods and
CC   compositions of the present invention are useful as therapeutic vaccine
CC   for cancer and for major viral infections, such as hepatoma and cervical
CC   cancer, that cause morbidity and mortality. They can also be used in
CC   treating animal diseases, such as equine herpesvirus, bovine viruses,
CC   Marek's disease, retroviral and lentiviral diseases and rabies, in the
CC   veterinary medicine context. The present sequence represents the
CC   nucleotide sequence of vector Sinrep5-E7-Hsp70 comprising the human
CC   papillomavirus (HPV) E7 antigenic protein and M. tuberculosis heat shock
CC   protein 70 (Hsp70) fusion sequence
XX
SQ   Sequence 12110 BP; 3339 A; 3084 C; 3137 G; 2550 T; 0 U; 0 Other;

  Query Match             89.4%;  Score 7637.4;  DB 6;  Length 12110;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7641;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
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Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
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Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
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Qy       3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
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Qy       3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
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Qy       4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
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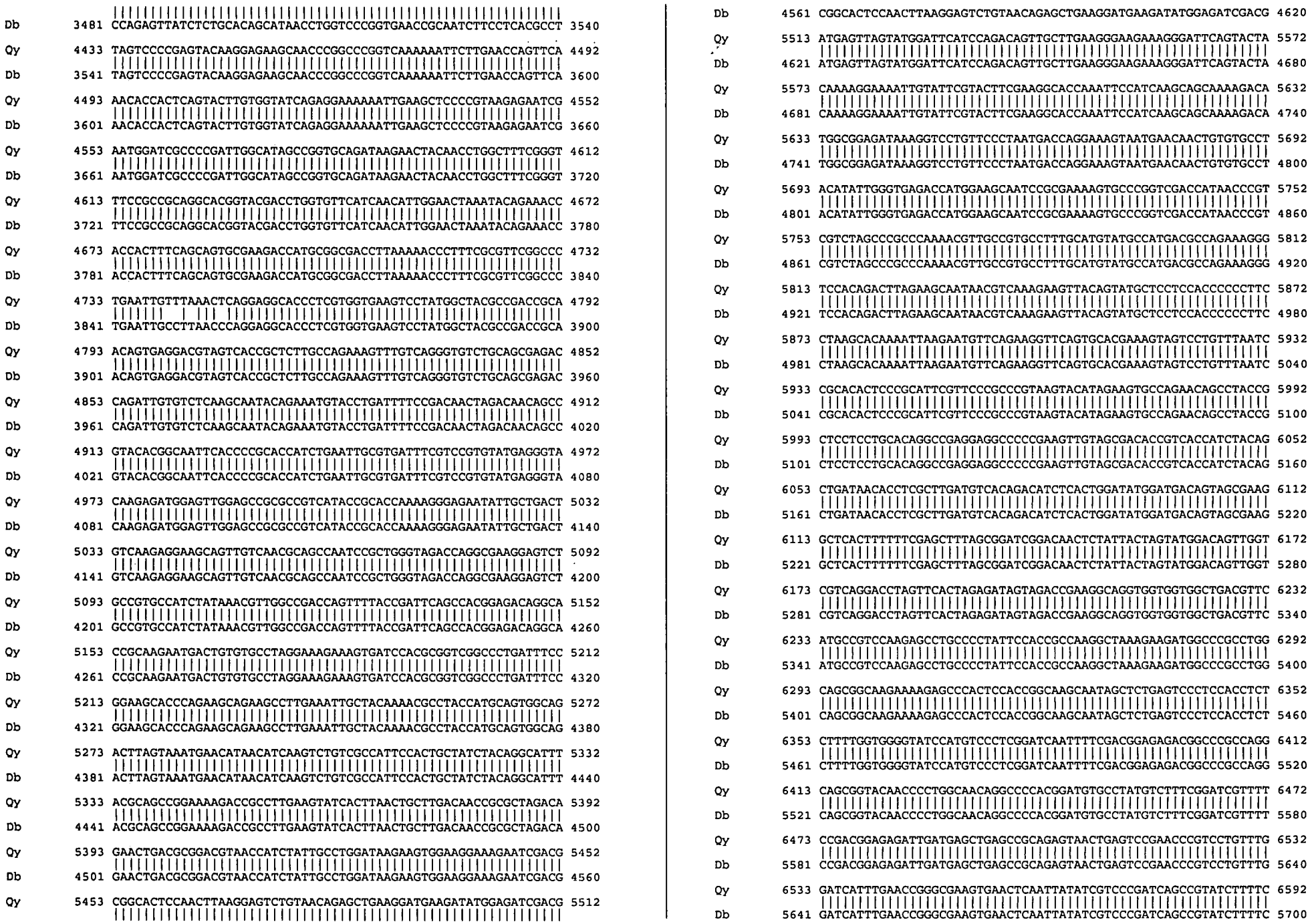
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Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 6300

Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 6360

Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 6420

Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6421 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 6480

Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540

Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6541 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 6600

Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6601 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 6660

Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6661 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 6720

Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6721 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 6780
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Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6781 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 6840

Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6841 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 6900

Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6901 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 6960

Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
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Db       6961 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7020

Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7021 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7080

Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 7140

Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7141 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 7200

Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7201 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 7260

Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 7320

Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 7380

Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 7440

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7441 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 7500

Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7501 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 7560

Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 7620

Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
             ||||||||||||||||||||||||||||
Db       7621 CTGACTAATACTACAACACCACCACCT 7647
```

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RESULT 14
AAX77358
ID   AAX77358 standard; DNA; 13905 BP.
XX
AC   AAX77358;
XX
DT   09-AUG-1999  (first entry)
XX
DE   Polynucleotide sequence of pTE5'2J.
XX
KW   Nucleic acid identification; exogenous protein; gene sorting;
KW   growth factor; membrane receptor; sindbis virus; ss.
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XX
OS Synthetic.
XX
PN WO9925876-A1.
XX
PD 27-MAY-1999.
XX
PF 17-NOV-1998; 98WO-US024520.
XX
PR 17-NOV-1997; 97US-00972218.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
XX
PI Bailey JE, Renner WA, Orberger GH, Koller D;
XX
DR WPI; 1999-357620/30.
XX
PT Isolating genes encoding proteins with selected properties, useful for
PT identifying therapeutic agents or targets.
XX
PS Disclosure; Fig 12A-D; 136pp; English.
XX
CC The invention relates to the identification of a recombinant nucleic acid
CC encoding an exogenous protein having a selected property. The method
CC comprises preparing a population of eukaryotic host cells, culturing the
CC cells under suitable conditions and identifying cells that contain the
CC recombinant nucleic acid. The method is used to sort genes according to
CC the type of proteins they express, and also to identify new ligand/
CC receptor interactions. Typical applications of the nucleic acid and the
CC exogenous protein are in isolation of new growth factors, cytokines,
CC membrane receptors, cytoplasmic, organelle or nuclear proteins, all of
CC which may be useful as therapeutic agents or therapeutic targets, e.g.
CC apoptosis-promoting or tumour suppressing proteins, regulators of cell
CC proliferation or metabolic processes etc. The protein can also be used to
CC screen for specific modulators. The nucleic acid can also be used as
CC sources of therapeutic antisense or ribozyme sequences. The method allows
CC the protein (rather than a partial DNA sequence) to be isolated and,
CC since a wide range of cells can be used, they can be expressed with the
CC correct glycosylation pattern
XX
SQ Sequence 13905 BP; 3931 A; 3551 C; 3440 G; 2983 T; 0 U; 0 Other;

Query Match 89.4%; Score 7637.4; DB 2; Length 13905;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
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Db        421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
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Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140

Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 1200

Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260

Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320

Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380

Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440

Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500
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Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560

Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620

Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740

Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 1800

Qy       2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
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Db       1801 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 1860

Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 1920

Qy       2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980

Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
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Db       1981 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2040

Qy       2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100

Qy       2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 2160

Qy       3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 2220

Qy       3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280

Qy       3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
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Db       2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340

Qy       3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400

Qy       3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 2460

Qy       3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 2520

Qy       3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 2580

Qy       3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 2640

Qy       3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700

Qy       3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 2760

Qy       3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820

Qy       3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
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Qy       3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
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Qy       4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
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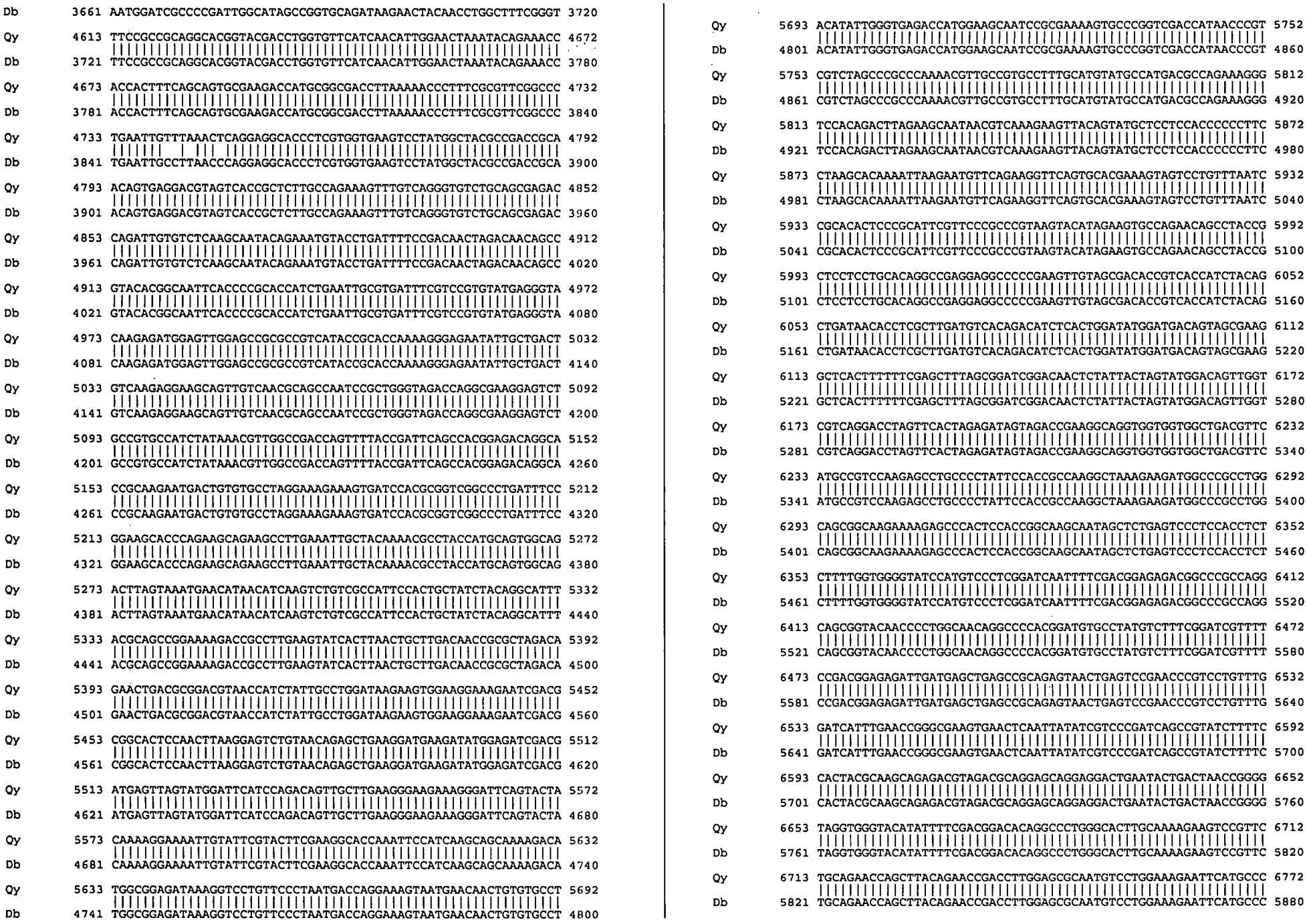
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RESULT 15
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ID   AAA90390 standard; DNA; 13905 BP.
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DT   10-JAN-2001  (first entry)
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DE   Plasmid pTE5'2J DNA sequence.
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KW   Nucleic acid identification; exogenous protein; drug screening;
KW   recombinant expression; pTE5'2J; cyclic; circular; ds.
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XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
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XX
DR WPI; 2000-551637/51.
XX
PT Identifying a recombinant nucleic acid to identify and isolate various
PT cellular proteins, comprises culturing a composition comprising
PT eukaryotic host cells and identifying a cell comprising recombinant
PT nucleic acid.
XX
PS Example; Fig 12A-D; 56pp; Japanese.
XX
CC The invention relates to the identification of a recombinant nucleic acid
CC encoding an exogenous protein having a selected property.The method
CC comprises preparing populations of eukaryotic host cells, where each cell
CC comprises an expression vector encoding a different exogenous protein.
CC The host cells are cultured under suitable conditions and the nucleic
CC acid which encodes the exogenous protein is identified. The method is
CC useful for the identification and isolation of proteins with a selected
CC property. Typical applications of the nucleic acid and the exogenous
CC protein are in isolation of new growth factors, cytokines, membrane
CC receptors, cytoplasmic, organelle or nuclear proteins, all of which may
CC be useful as therapeutic agents or therapeutic targets, e.g., pro-
CC apoptotic or tumour suppressing proteins, regulators of cell
CC proliferation or of metabolic processes. The protein can also be used to
CC screen for ligands and specific modulators of activity. The method of the
CC invention allows the direct cloning of full length cDNAs in one step. It
CC facilitates direct expression of the protein without the need to perform
CC further procedures such as subcloning and establishment of a cell line
CC for protein production. The method allows a protein of interest (rather
CC than a partial DNA sequence) to be isolated and, since a wide range of
CC cell types can be used, they can be expressed in a correctly folded and
CC glycosylated form. The present sequence represents plasmid pTE5'2J which
CC was used in the exemplifications of the invention. This patent is related
CC to WO9925876
XX
SQ Sequence 13905 BP; 3931 A; 3551 C; 3440 G; 2983 T; 0 U; 0 Other;

Query Match 89.4%; Score 7637.4; DB 3; Length 13905;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy       893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
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Db         1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy       953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
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Db        61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy      1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
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Db       121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy      1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
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Db       181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy      1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
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Db       241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy      1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
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Db       301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy      1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
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Qy      1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
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Qy      1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540

Qy      1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy      1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
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Qy      1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
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Qy      1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
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Db       901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

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Db       961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020

Qy      1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
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Db      1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140

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Qy      2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
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Db      1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560

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Qy      2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
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Qy      2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
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Db      2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100

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Qy      3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
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Db      2341 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400

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Qy      3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
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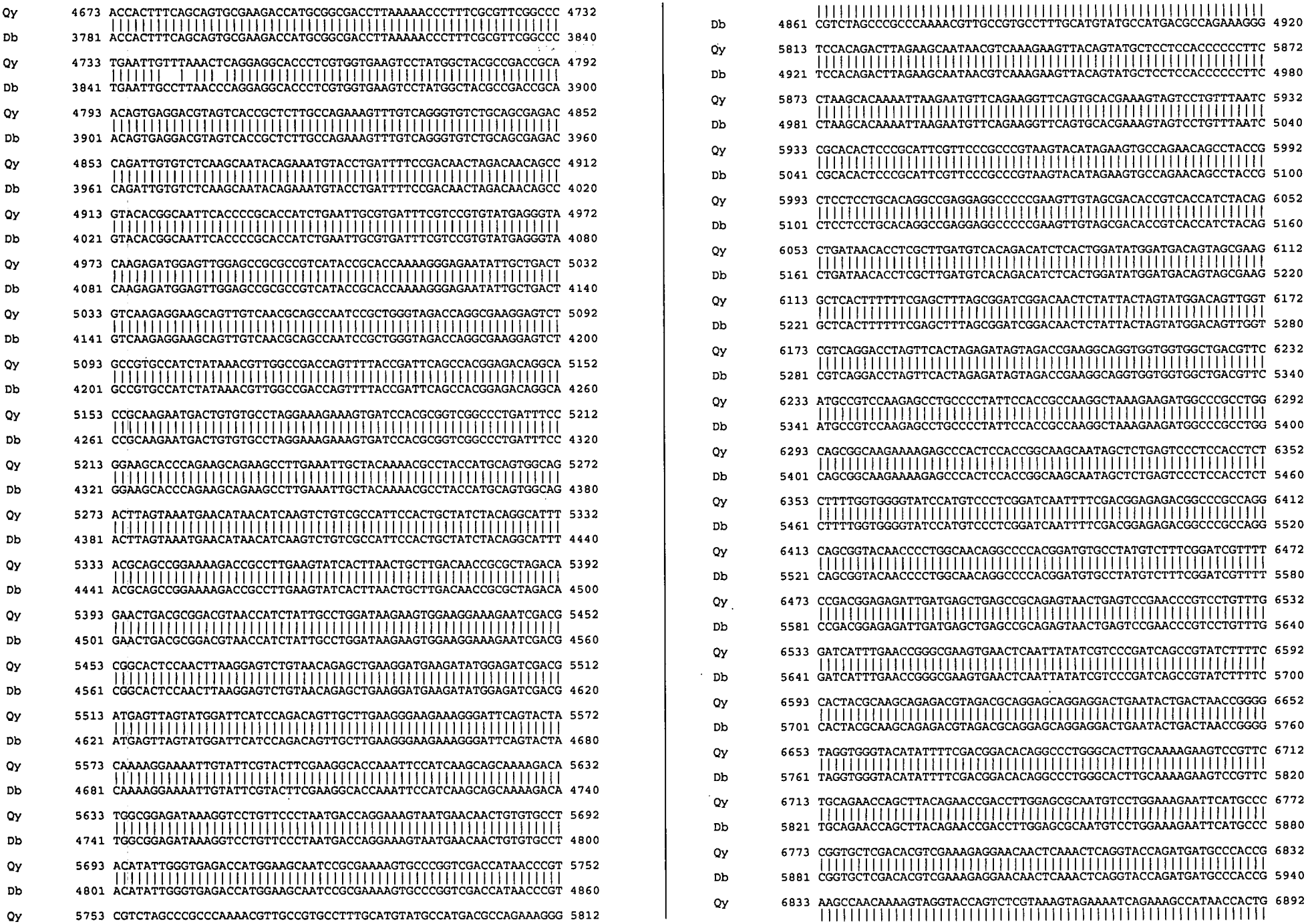
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Db 4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980
Qy 5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
Db 4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040
Qy 5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
Db 5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100
Qy 5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
Db 5101 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 5160
Qy 6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
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Db 5221 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280
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Db 5461 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 5520
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Qy 6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
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Db 5641 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 5700
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Qy 6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
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Qy 6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892

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Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
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